

GenCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM field - nucleic search, using sw model

Run on: November 20, 1999, 15:50:45 : Search time 308.23 seconds

(without alignments)
12120.749 Million cell updates/sec

Title: us-09-126-945-1

Percent score: 1894

Sequence: 1 atcgaattctctccacacac... .ataaagatactagaacatc 1894

Scoring table: IDENTITY_NUCGX

Sequence: 251572 seqs, 98525752 residues

Database:

EST:*

1: em_est11:*

2: em_est12:*

3: em_est13:*

4: em_est14:*

5: em_est15:*

6: em_est16:*

7: em_est17:*

8: em_est18:*

9: em_est19:*

10: em_est20:*

11: em_est21:*

12: em_est22:*

13: em_est23:*

14: em_est24:*

15: em_est25:*

16: em_est26:*

17: em_est27:*

18: em_est28:*

19: em_est29:*

20: em_est30:*

21: em_est31:*

22: em_est32:*

23: em_est33:*

24: em_est34:*

25: em_est35:*

26: em_est36:*

27: em_est37:*

28: em_est38:*

29: em_est39:*

30: em_est40:*

31: em_est41:*

32: em_est42:*

33: em_est43:*

34: em_est44:*

35: em_est45:*

36: em_est46:*

37: em_est47:*

38: em_est48:*

39: em_est49:*

40: em_est50:*

41: em_est51:*

42: em_est52:*

43: em_est53:*

44: em_est54:*

45: em_est55:*

46: em_est56:*

47: em_est57:*

48: em_est58:*

49: em_est59:*

50: em_est60:*

51: em_est61:*

52: em_est62:*

53: em_est63:*

54: em_est12:*

55: em_est13:*

56: em_est14:*

57: em_est15:*

58: em_est16:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
C 1	556	29.4	606	36	AA662164 ns66c07.s
C 2	509.2	28.9	514	36	AA662164 ns66c07.s
C 3	465.4	28.6	512	50	AA662164 ns66c07.s
C 4	374.8	19.8	392	36	AA662164 ns66c07.s
C 5	348.8	18.4	386	50	AA662164 ns66c07.s
C 6	325.2	17.2	366	36	AA662164 ns66c07.s
C 7	323.6	17.2	366	50	AA662164 ns66c07.s
C 8	317.6	16.8	355	34	AA662164 ns66c07.s
C 9	308.4	16.3	384	35	AA662164 ns66c07.s
C 10	291.2	15.4	369	30	AA662164 ns66c07.s
C 11	259.8	13.7	504	40	AA662164 ns66c07.s
C 12	236.2	12.5	441	50	AA662164 ns66c07.s
C 13	230.7	10.9	544	46	AA662164 ns66c07.s
C 14	180.2	9.5	390	22	AA662164 ns66c07.s
C 15	175.2	9.3	245	44	AA662164 ns66c07.s
C 16	174.8	9.2	216	43	AA662164 ns66c07.s
C 17	174.8	9.2	223	44	AA662164 ns66c07.s
C 18	174.8	9.2	222	44	AA662164 ns66c07.s
C 19	174.8	9.2	244	44	AA662164 ns66c07.s
C 20	174.8	9.2	232	44	AA662164 ns66c07.s
C 21	174.8	9.2	224	44	AA662164 ns66c07.s
C 22	174.8	9.2	199	44	AA662164 ns66c07.s
C 23	174.8	9.2	220	44	AA662164 ns66c07.s
C 24	174.8	9.2	218	44	AA662164 ns66c07.s
C 25	174.8	9.2	218	44	AA662164 ns66c07.s
C 26	174.8	9.2	231	44	AA662164 ns66c07.s
C 27	174.8	9.2	231	44	AA662164 ns66c07.s
C 28	174.8	9.2	222	44	AA662164 ns66c07.s
C 29	174.8	9.2	212	44	AA662164 ns66c07.s
C 30	174.8	9.2	220	44	AA662164 ns66c07.s
C 31	174.8	9.2	215	44	AA662164 ns66c07.s
C 32	174.8	9.2	227	44	AA662164 ns66c07.s
C 33	174.8	9.2	242	44	AA662164 ns66c07.s
C 34	174.8	9.2	242	44	AA662164 ns66c07.s
C 35	174.8	9.2	232	44	AA662164 ns66c07.s
C 36	174.8	9.2	228	44	AA662164 ns66c07.s
C 37	174.8	9.2	219	44	AA662164 ns66c07.s
C 38	174.8	9.2	217	45	AA662164 ns66c07.s
C 39	174.8	9.2	217	45	AA662164 ns66c07.s
C 40	174.8	9.2	217	45	AA662164 ns66c07.s
C 41	174.8	9.2	217	45	AA662164 ns66c07.s
C 42	174.8	9.2	234	44	AA662164 ns66c07.s
C 43	174.8	9.2	222	43	AA662164 ns66c07.s
C 44	173.8	9.2	218	43	AA662164 ns66c07.s
C 45	173.8	9.2	220	43	AA662164 ns66c07.s

ALIGNMENTS

RESULT 1

AA662164/c

DEFINITION

ns66c07.s1 MCI-GAP.Pr22 Homo sapiens cDNA clone IMAGE:118588 3' similar to SW-ETS4_PROME P29775 DNA-BINDING PROTEIN D-ETS-4 : mRNA

ACCESION

AA662164

NID

92616255

VERB: 4 AA662204.1 GI:2616255
 KEYWORDS: EST

Source: 1

Organism: Homo sapiens

Reference: Moravcsik Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

Reference: 1 (bases 1 to 514)

Accession: NC_000001

URL: <http://www.ncbi.nlm.nih.gov/ncicgap>

NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://lmi.gov/htbp/image.html>

Comment: This sequence version replaced gi:1392902.

Insert Length: 734 Std Error: 0.00
 Seq Primer: -28m13 rev1 ET from Amersham

High Quality Sequence Stop: 393.

Features: 1 (bases 1 to 514)

Accession: AA662204

Version: 1

Keywords: EST

Source: human

Organism: Homo sapiens

Reference: Moravcsik Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

Reference: 1 (bases 1 to 514)

Accession: NC_000001

URL: <http://www.ncbi.nlm.nih.gov/ncicgap>

NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://lmi.gov/htbp/image.html>

Comment: This sequence version replaced gi:1392902.

Insert Length: 734 Std Error: 0.00
 Seq Primer: -28m13 rev1 ET from Amersham

High Quality Sequence Stop: 393.

Features: 1 (bases 1 to 514)

Accession: AA662204

Version: 1

Keywords: EST

Source: human

Organism: Homo sapiens

Reference: Moravcsik Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

Reference: 1 (bases 1 to 514)

Accession: NC_000001

URL: <http://www.ncbi.nlm.nih.gov/ncicgap>

NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://lmi.gov/htbp/image.html>

Comment: This sequence version replaced gi:1392902.

Insert Length: 734 Std Error: 0.00
 Seq Primer: -28m13 rev1 ET from Amersham

High Quality Sequence Stop: 393.

Features: 1 (bases 1 to 514)

Accession: AA662204

Version: 1

Keywords: EST

Source: human

DB 1588 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1647

DB 1647 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1707

DB 1648 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1707

DB 248 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 186

DB 1708 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1767

DB 1768 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1827

DB 1769 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1827

DB 1828 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1886

DB 1887 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1894

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

DB 8 gtcctgagggcctcggagacacatgagcagggtgtctctctcagccacactc 1

Forquism - "Homo sapiens"

MAIL 2205876

```

/^\s*_id="NCI_CGAP_Ut3"
/^\s*_type="poorly-differentiated endometrial

```

adenocarcinoma, 2 pooled tumors"
/136_pos+ "PHIP"

/note "organ: uterus; Vector: pCMV-SPORT6; Site:
site 2: NotI; cloned unidirectionally. Primer:

Average insert size 1.45 kb. Life Technologies 11541-018"

104	113	90	1
q	q	t	others

17.18, Score 323.6; DB 50; Length 366;

Identity: 98.8%; Pred. NO. 1.3e-29;
 Score: 1.00; Mismatches: 4; Indels: 2;

1. The first part of the document is a title page. It contains the title of the document, the author's name, and the date of the document. The title is "The First Part of the Document". The author's name is "John Doe". The date is "12/12/2023".

ATGAGGACCACTG-CCNCAGGGGATATGGCTCCTCTGGG

tttgggcttggttttcctcctcaagccccaactatcctcccctgaagaagaa

[illegible]

Journal of Management Education

[illegible]

AACAGCCTGCGTGGATTTGTTC

CCCTTACCAAGGCCAACGCGAGTCACGGCCTCTCTCTGTCTCCCA

ATTGATTTGACAAAGGCCACAGGCACTCCAGGCTCTCTTTGCTCCA

at ttttaccacctgtcattgttcaggggacaatctgcacct

CAATTTCACACACGACATGCTGCAGGAGACATCTGCACCCCT

cttgcacatggtcgaataataaagataactagaagactg 189

CTATGATTCGCTGGGAATGCATAATAAGATACTAGAGAACTG 14

	EST	19-AUG-2006
MPNA	EST	
Homo sapiens CDNA clone IMAGE:948171		

101.251686

5015

Primates; Catarrhini; Hominoidea; Hominidae; Homo.

http://www.nobi.nlm.nih.gov/nclgap

Cancer Institute, Cancer Genome Anatomy Project
 Fred Hutchinson

101 (1997)

Robert Strausberg, Ph.D.
1946-1950

Robert_Straussberg@nih.gov

Richard K. Fimmerl-Buck, M.D., Ph.D., Rodrigo F.

Library Preparation: David B. Krizman, Ph.D.
Library Arranged by: Greg Lennon, Ph.D.

distributed by: Washington University Genome Sequencing Center
distribution: NCI-DCAP clone distribution information

Downloaded from <http://ajphaphysocpharm.sagepub.com/> at 11:01 11 November 2014

Locus: EST Gene ID: mRNA EST 044827-1997
 Description: HOMO ID: Homo sapiens cDNA clone IMAGE:119858 3'
 Similar to: SW:U94_0906 p29775 DNA-BINDING PROTEIN P-ETS-4.1, MPNNA
 sequence
 Accession: AF042244
 MID: 02610255
 Version: 06/07/97 11:27:0255
 Keywords: EST
 Source: Human
 Organism: Homo sapiens
 Eukaryote: Metazoa: Chordata: Craniata: Vertebrata: Mammalia:
 Eutheria: Primates: Catarrhini: Hominoidea: Homo.
 (bases 1 to 600)
 Reference: NCICAP <http://www.ncbi.nlm.nih.gov/ncicap>.
 Author(s): National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
 Title: Tumor Gene Index
 Journal: Imprint Issue (1997)
 Comment: On Sep. 12, 1996, this sequence version replaced g11392902.

[illegible]

FEATURES	source
Seq primer: -400P from GIBCO.	
Location/Qualifiers	
1. 441	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone_image="2253656"	
/clone_lib="NCI_CGAP_Pr28"	
/sex="male"	
/dev_stage="adult"	
/lab_host="DH10B"	
/note="Jordan, prostate. Vector: pT73D-Pac (Pharmacia)	
with a modified polylinker. Plasmid DNA from the	
normalized library NCI_CGAP_Pr22 was prepared, and 5S	
circles were made in vitro. Following HAP purification,	
this DNA was used as tracer in a subtractive hybridization	
reaction. The driver was PCR-amplified cDNAs from a pool	

ALIGNMENTS

RESULT 1
AA662164 606 bp mRNA EST 03-DEC-1997
18866097.st NCI-CGAP_F122 Homo sapiens cDNA clone IMAGE:118588 3'
DEFINITION similar to SW-ET54_PROMO P29775 DNA-BINDING PROTEIN D-ETS-4 ; mRNA

ACCESSION

AA662164

NID

AA662164

KEYWORDS

EST

SOURCE

human

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 606)

AUTHORS

Emmert-Buck, M.D., Ph.D.

TITL

NCI-CGAP

COMMENT

18866097.st

FEATURES

18866097.st

LOCUS

18866097.st

DEFINITION

18866097.st

ACCESSION

18866097.st

NID

18866097.st

KEYWORDS

EST

SOURCE

human

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 606)

AUTHORS

Emmert-Buck, M.D., Ph.D.

TITL

NCI-CGAP

COMMENT

18866097.st

FEATURES

18866097.st

LOCUS

18866097.st

DEFINITION

18866097.st

ACCESSION

18866097.st

NID

18866097.st

KEYWORDS

EST

SOURCE

human

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 606)

AUTHORS

Emmert-Buck, M.D., Ph.D.

TITL

NCI-CGAP

COMMENT

18866097.st

FEATURES

18866097.st

LOCUS

18866097.st

DEFINITION

18866097.st

ACCESSION

18866097.st

NID

18866097.st

KEYWORDS

EST

1408 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1468 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1469 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1468 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1469 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1468 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1469 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1468 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1469 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1468 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1469 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1468 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1469 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1468 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1469 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1468 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1469 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1468 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1469 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1468 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1469 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1468 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1469 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1468 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1469 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1468 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1469 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1468 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1469 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1468 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1469 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1468 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1469 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1468 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1469 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1468 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1469 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1468 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1469 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1468 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1469 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1468 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

1469 cctgcaccccatcctgagtcgctgagcccaaggcctgaaccgccctcagaagagctctc 1467

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced q1:1392997.

Insert Length: 734 Std Error: 0.00
Seq primer: -28m13 rev1 ET from Amerham.
Location/Qualifiers


```

Db 157 1577 ggggagataggggcctctgggggttcgggagccatgggggagggggtctctctctcaag 1616
|||||
Cc 418 ggggagataggggcctctgggggttcgggagccatgggggagggggtctctctctcaag 259
|||||
Qy 1637 ggggagataggggcctctgggggttcgggagccatgggggagggggtctctctctcaag 1636
|||||
Db 258 ggggagataggggcctctgggggttcgggagccatgggggagggggtctctctctcaag 199
|||||
Qy 1697 ggggagataggggcctctgggggttcgggagccatgggggagggggtctctctctcaag 1756
|||||
Db 198 ggggagataggggcctctgggggttcgggagccatgggggagggggtctctctctcaag 139
|||||
Qy 1757 ggggagataggggcctctgggggttcgggagccatgggggagggggtctctctctcaag 1816
|||||
Db 138 ggggagataggggcctctgggggttcgggagccatgggggagggggtctctctctcaag 79
|||||
Qy 1817 ggggagataggggcctctgggggttcgggagccatgggggagggggtctctctctcaag 1876
|||||
Db 78 ggggagataggggcctctgggggttcgggagccatgggggagggggtctctctctcaag 19
|||||
Qy 1877 ggggagataggggcctctgggggttcgggagccatgggggagggggtctctctctcaag 1894
|||||
Db 18 ggggagataggggcctctgggggttcgggagccatgggggagggggtctctctctcaag 1
|||||

RESULT 5
LOCUS A1685592 386 bp mRNA 27-MAY-1999
DEFINITION tu20c07.x1 NCI-CGAP_P128 Homo sapiens cDNA clone IMAGE:2251596 3'
sequence:
ACCESSION A1685592
VERSION 94896886
KEYWORDS A1685592.1 GI:4896886
SOURCE EST.
ORGANISM human.
REFERENCE Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia:
Eutheria: Primates: Catarrhini: Homiidae: Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jun 5, 1998 this sequence version replaced gi:4189477.

FEATURES
SOURCE
Seq primer: 400P from Gibco
High quality sequence stop: 380.
Location/Qualifiers
1..386
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:2251596"
/clone_lib="NCI-CGAP_P128"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/notes="Organ: Prostate; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI-CGAP_P128 was prepared, and ss

```

```

Db 157 1577 ggggagataggggcctctgggggttcgggagccatgggggagggggtctctctctcaag 1616
|||||
Cc 418 ggggagataggggcctctgggggttcgggagccatgggggagggggtctctctctcaag 259
|||||
Qy 1637 ggggagataggggcctctgggggttcgggagccatgggggagggggtctctctctcaag 1636
|||||
Db 258 ggggagataggggcctctgggggttcgggagccatgggggagggggtctctctctcaag 199
|||||
Qy 1697 ggggagataggggcctctgggggttcgggagccatgggggagggggtctctctctcaag 1756
|||||
Db 198 ggggagataggggcctctgggggttcgggagccatgggggagggggtctctctctcaag 139
|||||
Qy 1757 ggggagataggggcctctgggggttcgggagccatgggggagggggtctctctctcaag 1816
|||||
Db 138 ggggagataggggcctctgggggttcgggagccatgggggagggggtctctctctcaag 79
|||||
Qy 1817 ggggagataggggcctctgggggttcgggagccatgggggagggggtctctctctcaag 1876
|||||
Db 78 ggggagataggggcctctgggggttcgggagccatgggggagggggtctctctctcaag 19
|||||
Qy 1877 ggggagataggggcctctgggggttcgggagccatgggggagggggtctctctctcaag 1894
|||||
Db 18 ggggagataggggcctctgggggttcgggagccatgggggagggggtctctctctcaag 1
|||||

RESULT 5
LOCUS A1685592 386 bp mRNA 27-MAY-1999
DEFINITION tu20c07.x1 NCI-CGAP_P128 Homo sapiens cDNA clone IMAGE:2251596 3'
sequence:
ACCESSION A1685592
VERSION 94896886
KEYWORDS A1685592.1 GI:4896886
SOURCE EST.
ORGANISM human.
REFERENCE Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia:
Eutheria: Primates: Catarrhini: Homiidae: Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jun 5, 1998 this sequence version replaced gi:4189477.

FEATURES
SOURCE
Seq primer: 400P from Gibco
High quality sequence stop: 380.
Location/Qualifiers
1..386
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:2251596"
/clone_lib="NCI-CGAP_P128"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/notes="Organ: Prostate; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI-CGAP_P128 was prepared, and ss

```


Tue Nov 23 07:44:00 1999

us-09-126-945-1.rst

Page 31

[illegible]

Search completed. November 20, 1999, 15:57.13
Job time: 367 sec



OM search - cyclic search, using sw model

US-CG-126-945-1

Seagrass

Section 1.000

Sea: 1111

Date: _____

[illegible]

Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result	Query				Description
No.	Score	Match	Length	ID	

1	4.0	27.6	514	36	AA652204	AA712204	ns66c
2	349	18.4	384	50	AI685902	AI695902	ns70cc
3	284	15.0	386	35	AA545402	AA545402	ns74cc
4	284	15.0	392	36	AA639921	AA539921	ns84cc
5	287	13.0	355	34	AA513374	AA513374	ns94cc
6	220	12.1	366	35	AA652221	AA652221	ns99cc
7	143	9.1	215	43	AI223844	AI223844	gx11
8	9	9.1	223	44	AI270872	AI270872	gx57cc
9	113	9.1	222	44	AI271445	AI271445	gx59cc
10	113	9.1	244	44	AI275119	AI275119	gx66a3
11	113	9.1	234	44	AI275221	AI275221	gx66a3
12	113	9.1	223	44	AI284815	AI284815	gx55b8
13	113	9.1	199	44	AI289627	AI289627	gx52cc
14	113	9.1	220	44	AI289725	AI289725	gx42b
15	113	9.1	228	44	AI205465	AI205465	gx46b
16	113	9.1	218	44	AI205499	AI205499	gx46b
17	113	9.1	245	44	AI205522	AI205522	gx47b
18	113	9.1	231	44	AI205572	AI205572	gx48cc
19	113	9.1	231	44	AI205574	AI205574	gx48cc
20	113	9.1	222	44	AI205688	AI205688	gx48b
21	113	9.1	212	44	AI206749	AI206749	gx44a
22	113	9.1	220	44	AI206796	AI206796	gx44a
23	113	9.1	225	44	AI208614	AI208614	gx44a
24	113	9.1	227	44	AI208044	AI208044	gx46b
25	113	9.1	242	44	AI208888	AI208888	lts50b
26	113	9.1	242	44	AI208959	AI208959	lts48b
27	113	9.1	233	44	AI210659	AI210659	lts43cc
28	113	9.1	228	44	AI211359	AI211359	lts47g
29	113	9.1	219	44	AI211467	AI211467	lts44b
30	113	9.1	217	45	AI240387	AI240387	lts40b
31	113	9.1	217	45	AI240423	AI240423	lts40c
32	113	9.1	217	44	AI273150	AI273150	lts44
33	113	9.1	217	42	AI282370	AI282370	gx30cc
34	113	9.1	218	43	AI282370	AI282370	gx32a
35	113	9.1	237	43	AI282370	AI282370	gx32a
36	113	9.1	220	43	AI224659	AI224659	gx49a
37	113	9.1	218	44	AI250521	AI250521	gx37b
38	113	9.1	218	44	AI251136	AI251136	gx33b
39	113	9.1	247	44	AI255401	AI255401	gx55a
40	113	9.1	247	44	AI255404	AI255404	gx53a
41	113	9.1	218	44	AI270907	AI270907	gx51b
42	113	9.1	218	44	AI270910	AI270910	gx52a
43	113	9.1	218	44	AI270922	AI270922	gx52b
44	113	9.1	224	44	AI272143	AI272143	gx51a
45	113	9.1	219	44	AI272056	AI272056	gx52g

RESULT 1

AAG62204									
LOCUS	AA662204	514 bp	mRNA	EST	U3-DHC-1997				
DEFINITION	nslac6c07 r1 NC1_CAP_Prr2 Homo sapiens cDNA clone YACF11886R				5'				
	similar to SW.ETS4_DROME P29775 DNA-BINDING PROTEIN D. ETS_4 ; mRNA sequence.								
ACCSSION	AA662204								
CID	G2616295								

[illegible]

```

/Note="Organ: breast; Vector: PAMPl; mRNA made from breast carcinoma, cDNA made by oligo-dt priming. Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified."
BASE COUNT      76 a      58 c      55 g      33 t
ORIGIN

Query Match:      9.1%   Score 173;   E=44;   Length 220;
Best Local Similarity 100.0%;   Prod. No. 4.2e-77;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  1722  acgaaaggagagagctcagacaaaggacagagagagctcctctctgagagatc 1781
      |||
DB    10  ACAGAAAGGAGAGAGCTCAGCAAAAGGCAAGAGAGAGCTCTCTCTGATGATTC 69
      |||

OY  1782  cccgcctcccatctcgacacacacctgcgtatgtgaaggaggaagacctcgacacctaa 1841
      |||
DB    70  cccgcctcccatctcgacacacacctgcgtatgtgaaggaggaagacctcgacacctaa 129
      |||

OY  1842  ttggagcagcagagagtgccccgcggaatgataaagaatacctagagacta 1894
      |||
DB    130  ttggagcagcagagagtgccccgcggaatgataaagaatacctagagacta 182
      |||

RESULT 10
A1275319      244 bp      mRNA      EST      21-DEC-1998
LOCUS         GW56510.x1 NCI_CGAP_OV33 Homo sapiens cDNA clone IMAGE:1596026
DEFINITION   mRNA sequence.
ACCESSION    A1275319
NID          G3897593
VERSION      A1275319.1 GI:3897593
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    1 (bases 1 to 244)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
           Tumor Gene Index
           Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:1896026.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
CNA Library Preparation: David B. Krizman, Ph.D.
CNA Library Arrayed by: I M A G E Consortium, LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I M A G E Consortium/LLNL at:
www.bio.llnl.gov/dbfp/image/image.html

Insert length: 311      Std Error: 0.00
Seq primer: -400p from Gibco.
Location/Qualifiers
1..244
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1996026"
/clone_lib="NCI_CGAP_OV33"
/sex="female"
/tissue_type="borderline ovarian carcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/Note="Organ: Ovary; Vector: PAMPl; mRNA made from borderline ovarian carcinoma, cDNA made by oligo-dt priming. Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified."
BASE COUNT      84 a      65 c      57 g      38 t

```




GenScore version 4.5
Copyright 1994 Compugen Ltd

CM Protein - protein search using SW model

Run on November 20 1999 13:05:12 : Search time 15.75 seconds

(without alignments)
1309,023 Million cell updates/sec

Title: us-09-126-945-2

Percent Score: 35
1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Seq: 1 MGSASPGSLSSVSPSHLLPPDVT

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
Not defined by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
1	435	100.0	335	4	095238	095238	homo sapien
2	426	99.9	335	5	097145	097145	strongyloce
3	426	99.9	335	5	097145	097145	strongyloce
4	426	99.9	335	5	097145	097145	strongyloce
5	426	99.9	335	5	097145	097145	strongyloce
6	426	99.9	335	5	097145	097145	strongyloce
7	426	99.9	335	5	097145	097145	strongyloce
8	426	99.9	335	5	097145	097145	strongyloce
9	426	99.9	335	5	097145	097145	strongyloce
10	426	99.9	335	5	097145	097145	strongyloce
11	426	99.9	335	5	097145	097145	strongyloce
12	426	99.9	335	5	097145	097145	strongyloce
13	426	99.9	335	5	097145	097145	strongyloce
14	426	99.9	335	5	097145	097145	strongyloce
15	426	99.9	335	5	097145	097145	strongyloce
16	426	99.9	335	5	097145	097145	strongyloce
17	426	99.9	335	5	097145	097145	strongyloce
18	426	99.9	335	5	097145	097145	strongyloce
19	426	99.9	335	5	097145	097145	strongyloce
20	426	99.9	335	5	097145	097145	strongyloce
21	426	99.9	335	5	097145	097145	strongyloce
22	426	99.9	335	5	097145	097145	strongyloce
23	426	99.9	335	5	097145	097145	strongyloce
24	426	99.9	335	5	097145	097145	strongyloce
25	426	99.9	335	5	097145	097145	strongyloce
26	426	99.9	335	5	097145	097145	strongyloce
27	426	99.9	335	5	097145	097145	strongyloce
28	426	99.9	335	5	097145	097145	strongyloce
29	426	99.9	335	5	097145	097145	strongyloce
30	426	99.9	335	5	097145	097145	strongyloce
31	426	99.9	335	5	097145	097145	strongyloce
32	426	99.9	335	5	097145	097145	strongyloce
33	426	99.9	335	5	097145	097145	strongyloce
34	426	99.9	335	5	097145	097145	strongyloce
35	426	99.9	335	5	097145	097145	strongyloce
36	426	99.9	335	5	097145	097145	strongyloce
37	426	99.9	335	5	097145	097145	strongyloce
38	426	99.9	335	5	097145	097145	strongyloce
39	426	99.9	335	5	097145	097145	strongyloce
40	426	99.9	335	5	097145	097145	strongyloce
41	426	99.9	335	5	097145	097145	strongyloce
42	426	99.9	335	5	097145	097145	strongyloce
43	426	99.9	335	5	097145	097145	strongyloce
44	426	99.9	335	5	097145	097145	strongyloce
45	426	99.9	335	5	097145	097145	strongyloce

ALIGNMENTS

RESULT	ID	Query Match	Score	DB	Length	Mismatches	Conservative	0	Indels	0	Gaps	0
1	095238	100.0%	335	4	335	0	0	0	0	0	0	0
2	095238	100.0%	335	4	335	0	0	0	0	0	0	0
3	095238	100.0%	335	4	335	0	0	0	0	0	0	0
4	095238	100.0%	335	4	335	0	0	0	0	0	0	0
5	095238	100.0%	335	4	335	0	0	0	0	0	0	0
6	095238	100.0%	335	4	335	0	0	0	0	0	0	0
7	095238	100.0%	335	4	335	0	0	0	0	0	0	0
8	095238	100.0%	335	4	335	0	0	0	0	0	0	0
9	095238	100.0%	335	4	335	0	0	0	0	0	0	0
10	095238	100.0%	335	4	335	0	0	0	0	0	0	0
11	095238	100.0%	335	4	335	0	0	0	0	0	0	0
12	095238	100.0%	335	4	335	0	0	0	0	0	0	0
13	095238	100.0%	335	4	335	0	0	0	0	0	0	0
14	095238	100.0%	335	4	335	0	0	0	0	0	0	0
15	095238	100.0%	335	4	335	0	0	0	0	0	0	0
16	095238	100.0%	335	4	335	0	0	0	0	0	0	0
17	095238	100.0%	335	4	335	0	0	0	0	0	0	0
18	095238	100.0%	335	4	335	0	0	0	0	0	0	0
19	095238	100.0%	335	4	335	0	0	0	0	0	0	0
20	095238	100.0%	335	4	335	0	0	0	0	0	0	0
21	095238	100.0%	335	4	335	0	0	0	0	0	0	0
22	095238	100.0%	335	4	335	0	0	0	0	0	0	0
23	095238	100.0%	335	4	335	0	0	0	0	0	0	0
24	095238	100.0%	335	4	335	0	0	0	0	0	0	0
25	095238	100.0%	335	4	335	0	0	0	0	0	0	0
26	095238	100.0%	335	4	335	0	0	0	0	0	0	0
27	095238	100.0%	335	4	335	0	0	0	0	0	0	0
28	095238	100.0%	335	4	335	0	0	0	0	0	0	0
29	095238	100.0%	335	4	335	0	0	0	0	0	0	0
30	095238	100.0%	335	4	335	0	0	0	0	0	0	0
31	095238	100.0%	335	4	335	0	0	0	0	0	0	0
32	095238	100.0%	335	4	335	0	0	0	0	0	0	0
33	095238	100.0%	335	4	335	0	0	0	0	0	0	0
34	095238	100.0%	335	4	335	0	0	0	0	0	0	0
35	095238	100.0%	335	4	335	0	0	0	0	0	0	0
36	095238	100.0%	335	4	335	0	0	0	0	0	0	0
37	095238	100.0%	335	4	335	0	0	0	0	0	0	0
38	095238	100.0%	335	4	335	0	0	0	0	0	0	0
39	095238	100.0%	335	4	335	0	0	0	0	0	0	0
40	095238	100.0%	335	4	335	0	0	0	0	0	0	0
41	095238	100.0%	335	4	335	0	0	0	0	0	0	0
42	095238	100.0%	335	4	335	0	0	0	0	0	0	0
43	095238	100.0%	335	4	335	0	0	0	0	0	0	0
44	095238	100.0%	335	4	335	0	0	0	0	0	0	0
45	095238	100.0%	335	4	335	0	0	0	0	0	0	0

DI 1-MAY-1999 (TREMBLER). 10. Created)

DI 1-MAY-1999 (TREMBLER). 10. Last sequence update)

DI 1-MAY-1999 (TREMBLER). 10. Last annotation update)

DE ETS DOMAIN PROTEIN (FRAGMENT).

GN ETS.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OC Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

RN

PP SEQUENCE FROM N.A.

PA LIN J.H., SAITO T., ANDERSON D.J., LANCE-JONES C., JESSELL T.M., ARBER S.;

RT subtypes defined by coordinate ETS gene expression.

RT subtypes defined by coordinate ETS gene expression.

RL Cell 95:393-407(1998).

DR EMBL: AF075708; AAC97209.1; -

DR PROSITE: PS00345; ETS_DOMAIN_1; 1.

DR PROSITE: PS00346; ETS_DOMAIN_2; 1.

FT NON_TER

FT SEQUENCE 336 AA; 38518 MW; 92622020 CRC32;

Query Match 4.2% Score 14; DB 13; Length 236;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 KNRPMANNKLSRS 308
Db 238 KNRPMANNKLSRS 151

RESULT 9
ID 019695 PRELIMINARY; PRT: 477 AA.
AC 019695;
DT 01-NOV-1996 (TREMBLER). 01. Created)
DI 01-NOV-1996 (TREMBLER). 01. Last sequence update)
DI 01-NOV-1998 (TREMBLER). 08. Last annotation update)
DE SIMILAR TO DNA BINDING PROTEIN.
GN F22A3.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Phabditia; Phabditidae; Rhabditina; Rhabditidae; Rhabditidae; Pelodidae; Caenorhabditis.
RN

PP SEQUENCE FROM N.A.
PX MEDLINE: 94150718.
PA WILSON R., AINSWORTH P., ANDERSON K., RAYNES G., BEKES M., BONEFIELD J., BURTON J., CONNELL M., COOPER T., GUNSON A., CRAYTON M., DEAR S., DU Z., DUBBIN P., FAVELLO A., ELLON L., JONES M., KESHAW J., KIPSTEN J., LAISTER N., LAIBELLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE R., O'CALLAGHAN M., PAPSONS J., PERCY C., REKEN L., ROOPE A., SAINES D., SHAWNEEN R., SMALDON N., SMITH A., SONNHAMMER E., STADEN P., STILSON J., THIERY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOLDMAN P., 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
RL Nature 368:32-38(1994).

Query Match 4.2% Score 14; DB 13; Length 477;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 KNRPMANNKLSRS 308
Db 238 KNRPMANNKLSRS 392

RESULT 9
ID 019695 PRELIMINARY; PRT: 336 AA.
AC 019695;
DT 1-MAY-1999 (TREMBLER). 10. Created)
DI 1-MAY-1999 (TREMBLER). 10. Last sequence update)
DI 1-MAY-1999 (TREMBLER). 10. Last annotation update)
DE ETS DOMAIN PROTEIN (FRAGMENT).

GN PEAS.
OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OC Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

RN

PP SEQUENCE FROM N.A.

PA LIN J.H., SAITO T., ANDERSON D.J., LANCE-JONES C., JESSELL T.M., ARBER S.;

RT subtypes defined by coordinate ETS gene expression.

RT subtypes defined by coordinate ETS gene expression.

RL Cell 95:393-407(1998).

DR EMBL: AF075708; AAC97209.1; -

DR PROSITE: PS00345; ETS_DOMAIN_1; 1.

DR PROSITE: PS00346; ETS_DOMAIN_2; 1.

FT NON_TER

FT SEQUENCE 336 AA; 38518 MW; 92622020 CRC32;

Query Match 4.2% Score 14; DB 13; Length 336;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 KNRPMANNKLSRS 308
Db 238 KNRPMANNKLSRS 251

RESULT 9
ID 019695 PRELIMINARY; PRT: 532 AA.
AC 019695;
DT 01-NOV-1996 (TREMBLER). 01. Created)
DI 01-NOV-1996 (TREMBLER). 01. Last sequence update)
DI 01-NOV-1998 (TREMBLER). 08. Last annotation update)
DE SIMILAR TO DNA BINDING PROTEIN.
GN F22A3.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Phabditia; Phabditidae; Rhabditina; Rhabditidae; Rhabditidae; Pelodidae; Caenorhabditis.
RN

PP SEQUENCE FROM N.A.
PX MEDLINE: 94150718.
PA WILSON R., AINSWORTH P., ANDERSON K., RAYNES G., BEKES M., BONEFIELD J., BURTON J., CONNELL M., COOPER T., GUNSON A., CRAYTON M., DEAR S., DU Z., DUBBIN P., FAVELLO A., ELLON L., JONES M., KESHAW J., KIPSTEN J., LAISTER N., LAIBELLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE R., O'CALLAGHAN M., PAPSONS J., PERCY C., REKEN L., ROOPE A., SAINES D., SHAWNEEN R., SMALDON N., SMITH A., SONNHAMMER E., STADEN P., STILSON J., THIERY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOLDMAN P., 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
RL Nature 368:32-38(1994).

Query Match 2.7% Score 9; DB 5; Length 532;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 MNRDKLSRS 308



GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

CM is a protein search using sw model

Run: November 20 1999, 18:07:15 Search time 11.23 Seconds

(without alignments)
1195.186 Million cell updates/sec

US-09-126-945-2

Performance: 335
1 MOSASPOLSVSPSHLLP
GIRKPOLSVPLVGVHPVPI 335

Score: 122810

Search: 122810 seqs, 40055486 residues

Database: PIR-600*

1: PIR1*
2: PIR2*
3: PIR3*
4: PIR4*

Print: No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is printed by analysis of the total score distribution

SUMMARIES

Res. No. Score Copy Match Length DB ID

Description

Res. No.	Score	Copy	Match	Length	DB	ID	Description
1	4	7	2	114	2	S28821	transcription factor
2	4	4	2	477	1	I38893	transcription factor
3	4	4	2	477	1	B45396	transcription factor
4	4	4	2	510	1	S45692	transcription factor
5	4	4	2	462	1	S28821	transcription factor
6	4	4	2	555	1	S24061	transcription factor
7	4	4	2	453	2	B42093	serum response fac
8	4	4	2	430	2	I48755	MSAP1 - mouse
9	4	4	2	405	2	A42093	transcription fac
10	4	4	2	486	1	TVHUEG	transcription prote
11	4	4	2	478	1	S60754	transcription fac
12	4	4	2	452	1	I37565	transcription prote
13	4	4	2	452	1	S29844	transcription prote
14	4	4	2	452	1	S17403	transcription prote
15	4	4	2	452	1	S49013	transcription prote
16	4	4	2	452	1	TVHUEK	transcription prote
17	4	4	2	452	1	S28821	transcription fac
18	4	4	2	452	1	S28821	transcription fac
19	4	4	2	452	1	S28821	transcription fac
20	4	4	2	452	1	S28821	transcription fac
21	4	4	2	452	1	S28821	transcription fac
22	4	4	2	452	1	S28821	transcription fac
23	4	4	2	452	1	S28821	transcription fac
24	4	4	2	452	1	S28821	transcription fac
25	4	4	2	452	1	S28821	transcription fac
26	4	4	2	452	1	S28821	transcription fac
27	4	4	2	452	1	S28821	transcription fac
28	4	4	2	452	1	S28821	transcription fac
29	4	4	2	452	1	S28821	transcription fac
30	4	4	2	452	1	S28821	transcription fac
31	4	4	2	452	1	S28821	transcription fac
32	4	4	2	452	1	S28821	transcription fac
33	4	4	2	452	1	S28821	transcription fac
34	4	4	2	452	1	S28821	transcription fac
35	4	4	2	452	1	S28821	transcription fac
36	4	4	2	452	1	S28821	transcription fac
37	4	4	2	452	1	S28821	transcription fac
38	4	4	2	452	1	S28821	transcription fac
39	4	4	2	452	1	S28821	transcription fac
40	4	4	2	452	1	S28821	transcription fac
41	4	4	2	452	1	S28821	transcription fac
42	4	4	2	452	1	S28821	transcription fac
43	4	4	2	452	1	S28821	transcription fac
44	4	4	2	452	1	S28821	transcription fac
45	4	4	2	452	1	S28821	transcription fac

Query Match	Score	DB	Length	Best Local Similarity	Pred. No.	Matches	Conservative	Mismatches	Indels	Gaps
1	7.28	24	114	100.0%	3	24	0	0	0	0
2	7.28	24	114	100.0%	3	24	0	0	0	0
3	7.28	24	114	100.0%	3	24	0	0	0	0
4	7.28	24	114	100.0%	3	24	0	0	0	0
5	7.28	24	114	100.0%	3	24	0	0	0	0
6	7.28	24	114	100.0%	3	24	0	0	0	0
7	7.28	24	114	100.0%	3	24	0	0	0	0
8	7.28	24	114	100.0%	3	24	0	0	0	0
9	7.28	24	114	100.0%	3	24	0	0	0	0
10	7.28	24	114	100.0%	3	24	0	0	0	0
11	7.28	24	114	100.0%	3	24	0	0	0	0
12	7.28	24	114	100.0%	3	24	0	0	0	0
13	7.28	24	114	100.0%	3	24	0	0	0	0
14	7.28	24	114	100.0%	3	24	0	0	0	0
15	7.28	24	114	100.0%	3	24	0	0	0	0
16	7.28	24	114	100.0%	3	24	0	0	0	0
17	7.28	24	114	100.0%	3	24	0	0	0	0
18	7.28	24	114	100.0%	3	24	0	0	0	0
19	7.28	24	114	100.0%	3	24	0	0	0	0
20	7.28	24	114	100.0%	3	24	0	0	0	0
21	7.28	24	114	100.0%	3	24	0	0	0	0
22	7.28	24	114	100.0%	3	24	0	0	0	0
23	7.28	24	114	100.0%	3	24	0	0	0	0
24	7.28	24	114	100.0%	3	24	0	0	0	0
25	7.28	24	114	100.0%	3	24	0	0	0	0
26	7.28	24	114	100.0%	3	24	0	0	0	0
27	7.28	24	114	100.0%	3	24	0	0	0	0
28	7.28	24	114	100.0%	3	24	0	0	0	0
29	7.28	24	114	100.0%	3	24	0	0	0	0
30	7.28	24	114	100.0%	3	24	0	0	0	0
31	7.28	24	114	100.0%	3	24	0	0	0	0
32	7.28	24	114	100.0%	3	24	0	0	0	0
33	7.28	24	114	100.0%	3	24	0	0	0	0
34	7.28	24	114	100.0%	3	24	0	0	0	0
35	7.28	24	114	100.0%	3	24	0	0	0	0
36	7.28	24	114	100.0%	3	24	0	0	0	0
37	7.28	24	114	100.0%	3	24	0	0	0	0
38	7.28	24	114	100.0%	3	24	0	0	0	0
39	7.28	24	114	100.0%	3	24	0	0	0	0
40	7.28	24	114	100.0%	3	24	0	0	0	0
41	7.28	24	114	100.0%	3	24	0	0	0	0
42	7.28	24	114	100.0%	3	24	0	0	0	0
43	7.28	24	114	100.0%	3	24	0	0	0	0
44	7.28	24	114	100.0%	3	24	0	0	0	0
45	7.28	24	114	100.0%	3	24	0	0	0	0

ALIGNMENTS

RESULT 1
S28821
transcription factor ets-98B - fruit fly (Drosophila melanogaster) (fragment)
N:Alternate names: transforming protein ets-4
C:Species: Drosophila melanogaster
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 24-Sep-1998
C:Accession: S28821
R:Chen, T.; Bunting, M.; Karim, F.D.; Thummel, C.S.
Dev. Biol. 151, 176-191, 1992
A:Title: Isolation and characterization of five Drosophila genes that encode an ets-r
A:Reference number: S28821, NCBI:92249640
A:Accession: S28821
A:Molecule type: DNA
A:Residues: 1-114 <CHR>
A:Cross-references: EMBL:M86474, NID:9157195, PIR:9157196
C:Genetics:
A:Gene: Ets98B
A:Cross-references: FlyBase:FBgn0005659
C:Superfamily: ets DNA-binding domain homology
C:Keywords: DNA binding; nucleus; transcription factor
F:28-109/Domain: ets DNA-binding domain homology <ETS>

Query Match 7.28, Score 24, DB 2, Length 114
Best Local Similarity 100.0%, Pred. No. 3, 2e-17
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0

29 294 PKRPAMNDKLSFSPYKKGI 317
Db 71 RKRPMNDKLSFSPYKKGI 94

RESULT 2
I38893
transcription factor ER81 - human
N:Alternate names: ets translocation variant 1
C:Species: Homo sapiens (man)
C:Date: 01-Nov-1996 #sequence_revision 23-May-1997 #text_change 18-Sep-1998
C:Accession: I38893, S61541
R:From, I.S.; Davis, J.N.; Raza, B.S.; Sublett, J.F.; Foyse, M.F.; Downy, C.T.; Sh
Oncogene 10, 1229-1234, 1995
A:Title: A variant Ewing's sarcoma translocation (7;22) fuses the EWS gene to the ETS
A:Reference number: I38893, NCBI:3615084
A:Accession: I38893
A:Status: preliminary; translated from CB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-477 <RES>
A:Cross-references: EMBL:U17163, NID:9157195, PIR:9157196
R:From, D.; Gottle, L.; Baert, J.L.; Angell, L.; Stoppin, D.; de Lamoignon, Y.
Oncogene 11, 771-779, 1996
A:Title: Molecular characterization of the ets-related human transcription factor ER8
A:Reference number: S61541, MUID:95380185
A:Accession: S61541
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-39, VV, AG, 60, VV, 60, 116, VV, 118, 126, VV, 129, 252, 274, 349, VV, 360-477 <MO
A:Cross-references: EMBL:X87175, NID:91045066, PIR:91045061
C:Genetics:
A:Gene: GDB:ETV1
A:Cross-references: GDB:33229, OMIM:600541
A:Map position: 21q22.3-21q22.3
C:Superfamily: transcription factor ER81 ets DNA-binding domain homology

C:Keywords: DNA binding nucleus; transcription factor
 F143417/Domain: ets DNA-binding domain homology <ETS>

Query Match 4.2% Score 14; DB 1; Length 477;
 Best Local Similarity 100.0%; Pred. No. 2.6e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 295 KNRPMNYDKLSRS 408
 |||||
 DB 456 KNRPMNYDKLSRS 492

RESULT

A:Accession: S35534
 A:Residues: 1-462 <HIG>
 A:Cross-References: DB:012765; NID:921410; P11091-00720; P109219611
 C:Genetics:
 A:Gene: GDB:ETV4, EIA-F
 A:Cross-References: GDB:512230; OMIM:600711
 A:Map position: 17621-17921
 C:Superfamily: transcription factor ER81; ets DNA-binding domain homology
 C:Keywords: DNA binding; nucleus; transcription factor
 F:321-399/Domain: ets DNA-binding domain homology <ETS>

Query Match 4.2% Score 14; DB 1; Length 477;
 Best Local Similarity 100.0%; Pred. No. 2.6e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 295 KNRPMNYDKLSRS 408
 |||||
 DB 456 KNRPMNYDKLSRS 492

RESULT

A:Accession: S4692
 A:Residues: 1-555 <XIN>
 A:Cross-References: EMBL:X63190; NID:954627; P1093628
 C:Superfamily: transcription factor ER81; ets DNA-binding domain homology
 C:Keywords: DNA binding; nucleus; transcription factor
 F:414-492/Domain: ets DNA-binding domain homology <ETS>

Query Match 4.2% Score 14; DB 1; Length 510;
 Best Local Similarity 100.0%; Pred. No. 2.8e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 295 KNRPMNYDKLSRS 408
 |||||
 DB 456 KNRPMNYDKLSRS 492

RESULT 5
 S35534
 adenovirus E1A enhancer-binding protein E1A - human (fragment)

N:Alternate names: ets translocation variant 4
 C:Species: Homo sapiens (man)
 C:Date: 09-Dec-1993 #sequence_revision 23-May-1997 #text_change 18-Sep-1998

C:Accession: S35534
 R:Hisashino, F.; Yoshida, K.; Fujinaga, Y.; Kamio, K.; Fujinaga, K.
 Nucleic Acids Res. 21, 547-553, 1993

A:Title: Isolation of a cDNA encoding the adenovirus E1A enhancer binding protein: a
 A:Reference number: S35534; MIM:93181246
 A:Accession: S35534

A>Status: preliminary
 A:Molecule type: mRNA

A:Residues: 1-462 <HIG>
 A:Cross-References: DB:012765; NID:921410; P11091-00720; P109219611
 C:Genetics:

A:Gene: GDB:ETV4, EIA-F
 A:Cross-References: GDB:512230; OMIM:600711

A:Map position: 17621-17921
 C:Superfamily: transcription factor ER81; ets DNA-binding domain homology

C:Keywords: DNA binding; nucleus; transcription factor
 F:321-399/Domain: ets DNA-binding domain homology <ETS>

Query Match 4.2% Score 14; DB 1; Length 462;
 Best Local Similarity 100.0%; Pred. No. 2.6e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 295 KNRPMNYDKLSRS 308
 |||||
 DB 363 KNRPMNYDKLSRS 376

RESULT 6

A:Accession: S24061
 A:Residues: 1-555 <XIN>
 A:Cross-References: EMBL:X63190; NID:954627; P1093628
 C:Superfamily: transcription factor ER81; ets DNA-binding domain homology
 C:Keywords: DNA binding; nucleus; transcription factor
 F:414-492/Domain: ets DNA-binding domain homology <ETS>

Query Match 4.2% Score 14; DB 1; Length 555;
 Best Local Similarity 100.0%; Pred. No. 3e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 295 KNRPMNYDKLSRS 308
 |||||
 DB 456 KNRPMNYDKLSRS 469

RESULT 7

B42093
 serum response factor accessory protein-1 form a (sAP-1a) - human
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Aug-1998
 C:Accession: B42093; S28817
 C:Keywords: DNA binding; nucleus; transcription factor
 C:Keywords: DNA binding; nucleus; transcription factor
 F:414-492/Domain: ets DNA-binding domain homology <ETS>

A:Note: sequence extracted from NCBI backbone (NCBI:119390, NCBI:119392)
 A:Accession: 154170, MIM:193063, PID:q1000864
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 156 <RES>
 A:Cross-references: GB L47616, NIT 2100983, PID:q1000864
 A:Gene: GDB:FLI1
 A:Cross-references: GDB 127565, OMIM:193067
 A:Map position: 11q24.1-11q24.3
 A:Introns: 7/73
 C:Superfamily: transcription factor erf; ets DNA-binding domain homology; ets RII reg
 C:Keywords: alternative splicing; DNA binding; nucleus; proto-oncogene; transcription
 F:118-192/Domain: ets RII regulatory region homology <ERS>
 F:281-361/Domain: ets DNA-binding domain homology <ERS>

Query Match 2.4% Score 8; DB 1; Length 478;
 Best Local Similarity 100.0%; Pred. No. 4.2;
 Mismatches 0; Conservative 0; Indels 0; Gaps 0;

DB 300 MNYDKLSR 307
 330 MNYDKLSR 337

RESULT 13
 Transforming protein flt, short splice form - human
 N:Alternate names: Friend leukemia integration protein 1; transcription factor ERGB
 C:Species: Homo sapiens (man)
 C:Date: 02-Dec-1993 #sequence-revision 03-May-1997 #text-change 02-Sep-1997
 F:Accession: S29844
 F:Cross-references: EMBL:U03255; NID:q18265; PID:q18265
 F:Residues: 1-385 <HRO>
 A:Note: The authors have submitted the EMBL Data Library, May 1992
 A:Gene: GDB:FLI1
 A:Cross-references: GDB 127565, OMIM:193067
 A:Map position: 11q24.1-11q24.3
 C:Superfamily: transcription factor erf; ets DNA-binding domain homology; ets RII reg
 C:Keywords: alternative splicing; DNA binding; nucleus; proto-oncogene; transcription
 F:52-132/Domain: ets RII regulatory region homology <ERS>
 F:217-295/Domain: ets DNA-binding domain homology <ERS>

Query Match 2.4% Score 8; DB 1; Length 385;
 Best Local Similarity 100.0%; Pred. No. 3.4;
 Mismatches 0; Conservative 0; Indels 0; Gaps 0;

DB 300 MNYDKLSR 307
 264 MNYDKLSR 271

RESULT 14
 Transforming protein flt - mouse
 N:Alternate names: Friend leukemia integration protein 1; transcription factor ERGB
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1993 #sequence-revision 31-Dec-1993 #text-change 05-Sep-1997
 A:Accession: S17403

A:Note: sequence extracted from NCBI backbone (NCBI:119390, NCBI:119392)
 A:Accession: 154170, MIM:193063, PID:q1000864
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 156 <RES>
 A:Cross-references: GB L47616, NIT 2100983, PID:q1000864
 A:Gene: GDB:FLI1
 A:Cross-references: GDB 127565, OMIM:193067
 A:Map position: 11q24.1-11q24.3
 A:Introns: 7/73
 C:Superfamily: transcription factor erf; ets DNA-binding domain homology; ets RII reg
 C:Keywords: alternative splicing; DNA binding; nucleus; proto-oncogene; transcription
 F:118-192/Domain: ets RII regulatory region homology <ERS>
 F:281-361/Domain: ets DNA-binding domain homology <ERS>

Query Match 2.4% Score 8; DB 1; Length 478;
 Best Local Similarity 100.0%; Pred. No. 4.2;
 Mismatches 0; Conservative 0; Indels 0; Gaps 0;

DB 300 MNYDKLSR 307
 330 MNYDKLSR 337

RESULT 13
 Transforming protein flt, short splice form - human
 N:Alternate names: Friend leukemia integration protein 1; transcription factor ERGB
 C:Species: Homo sapiens (man)
 C:Date: 02-Dec-1993 #sequence-revision 03-May-1997 #text-change 02-Sep-1997
 F:Accession: S29844
 F:Cross-references: EMBL:U03255; NID:q18265; PID:q18265
 F:Residues: 1-385 <HRO>
 A:Note: The authors have submitted the EMBL Data Library, May 1992
 A:Gene: GDB:FLI1
 A:Cross-references: GDB 127565, OMIM:193067
 A:Map position: 11q24.1-11q24.3
 C:Superfamily: transcription factor erf; ets DNA-binding domain homology; ets RII reg
 C:Keywords: alternative splicing; DNA binding; nucleus; proto-oncogene; transcription
 F:52-132/Domain: ets RII regulatory region homology <ERS>
 F:217-295/Domain: ets DNA-binding domain homology <ERS>

Query Match 2.4% Score 8; DB 1; Length 385;
 Best Local Similarity 100.0%; Pred. No. 3.4;
 Mismatches 0; Conservative 0; Indels 0; Gaps 0;

DB 300 MNYDKLSR 307
 264 MNYDKLSR 271

RESULT 14
 Transforming protein flt - mouse
 N:Alternate names: Friend leukemia integration protein 1; transcription factor ERGB
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1993 #sequence-revision 31-Dec-1993 #text-change 05-Sep-1997
 A:Accession: S17403

A:Note: sequence extracted from NCBI backbone (NCBI:119390, NCBI:119392)
 A:Accession: 154170, MIM:193063, PID:q1000864
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 156 <RES>
 A:Cross-references: GB L47616, NIT 2100983, PID:q1000864
 A:Gene: GDB:FLI1
 A:Cross-references: GDB 127565, OMIM:193067
 A:Map position: 11q24.1-11q24.3
 A:Introns: 7/73
 C:Superfamily: transcription factor erf; ets DNA-binding domain homology; ets RII reg
 C:Keywords: alternative splicing; DNA binding; nucleus; proto-oncogene; transcription
 F:118-192/Domain: ets RII regulatory region homology <ERS>
 F:281-361/Domain: ets DNA-binding domain homology <ERS>

Query Match 2.4% Score 8; DB 1; Length 478;
 Best Local Similarity 100.0%; Pred. No. 4.2;
 Mismatches 0; Conservative 0; Indels 0; Gaps 0;

DB 300 MNYDKLSR 307
 330 MNYDKLSR 337

RESULT 13
 Transforming protein flt, short splice form - human
 N:Alternate names: Friend leukemia integration protein 1; transcription factor ERGB
 C:Species: Homo sapiens (man)
 C:Date: 02-Dec-1993 #sequence-revision 03-May-1997 #text-change 02-Sep-1997
 F:Accession: S29844
 F:Cross-references: EMBL:U03255; NID:q18265; PID:q18265
 F:Residues: 1-385 <HRO>
 A:Note: The authors have submitted the EMBL Data Library, May 1992
 A:Gene: GDB:FLI1
 A:Cross-references: GDB 127565, OMIM:193067
 A:Map position: 11q24.1-11q24.3
 C:Superfamily: transcription factor erf; ets DNA-binding domain homology; ets RII reg
 C:Keywords: alternative splicing; DNA binding; nucleus; proto-oncogene; transcription
 F:52-132/Domain: ets RII regulatory region homology <ERS>
 F:217-295/Domain: ets DNA-binding domain homology <ERS>

Query Match 2.4% Score 8; DB 1; Length 385;
 Best Local Similarity 100.0%; Pred. No. 3.4;
 Mismatches 0; Conservative 0; Indels 0; Gaps 0;

DB 300 MNYDKLSR 307
 264 MNYDKLSR 271

RESULT 14
 Transforming protein flt - mouse
 N:Alternate names: Friend leukemia integration protein 1; transcription factor ERGB
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1993 #sequence-revision 31-Dec-1993 #text-change 05-Sep-1997
 A:Accession: S17403

40 7 2.1 461 2 A69984 endo-1,4-beta-gluc
41 7 2.1 676 2 H70905 Probable 110D prot
42 7 2.1 686 2 A44842 CGMP-gated ion cha
43 7 2.1 144 2 I37382 CGMP-gated cation
44 7 2.1 723 2 SC4256 glycoprotein 3C -
45 7 2.1 411 2 A49127 homeotic protein A

ALIGNMENTS

RESULT 1

S28621 Transcription factor ets-ERM - fruit fly (Drosophila melanogaster) (fragment)

N:Alternative names: Transforming protein ets-4

C:Species: Drosophila melanogaster

C:Date: 31-Dec-1994 #sequence_revision 31-Dec-1993 #text_change 24-Sep-1998

C:Accession: S28621

R:Clon: 133 (Manning, M.; Karin, F.; Thummel, C.S.

Dev. Biol. 151, 176-191, 1992)

Att: Isolation and characterization of five Drosophila genes that encode an ets-rela

A:Reference number: S28621; MIM:92249640

A:Accession: S28621

A:Molecule type: DNA

A:Residues: 1114 (CHD)

A:Cross-references: EMBL:M84474; NID:q157195; PID:q157196

C:Gene name

A:Gene: ERM44P

A:Cross-references: EMBL:M84474; NID:q157195; PID:q157196

C:Superfamily: ets DNA-binding domain homology

C:Keywords: DNA binding; nucleus; transcription factor

F:291-1-92 (Manning, M.; Karin, F.; Thummel, C.S.)

Query Match 7.2% Score 24; DB 2; Length 114;

Best Local Similarity 100.0%; Pred. No. 3, 2e-17;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 KNPAMNYDKLSRS 317

DB 41 KNPAMNYDKLSRS 94

RESULT 2

S43692

N:Alternative names: ets variant gene 5; ets-related molecule

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 23-May-1997 #text_change 18-Sep-1998

C:Accession: S43692

R:Clon: 133 (Manning, M.; Karin, F.; Thummel, C.S.

Dev. Biol. 151, 176-191, 1992)

Att: Isolation and characterization of five Drosophila genes that encode an ets-rela

A:Reference number: S43692; MIM:94203669

A:Accession: S43692

A:Molecule type: mRNA

A:Residues: 1-510 (KON)

A:Cross-references: EMBL:X76184; NID:q479166; PID:q479167

C:Gene name

A:Gene: ERM44P

A:Cross-references: EMBL:X76184; NID:q479166; PID:q479167

C:Superfamily: ets DNA-binding domain homology

C:Keywords: DNA binding; nucleus; transcription factor

F:370-448/Domain: ets DNA-binding domain homology <ETS>

Query Match 4.2% Score 14; DB 1; Length 510;

Best Local Similarity 100.0%; Pred. No. 2, 4e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 KNPAMNYDKLSRS 308

DB 412 KNPAMNYDKLSRS 425

C:Superfamily: ets DNA-binding domain homology

C:Keywords: DNA binding; nucleus; transcription factor

F:337-415/Domain: ets DNA-binding domain homology <ETS>

Query Match 4.2% Score 14; DB 1; Length 477;

Best Local Similarity 100.0%; Pred. No. 2, 6e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 KNPAMNYDKLSRS 308

DB 379 KNPAMNYDKLSRS 392

RESULT 3

B46396 Transcription factor ERM1 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 19-May-1994 #sequence_revision 23-May-1997 #text_change 05-Sep-1997

C:Accession: B46396

R:Brown, T.A.; McKnight, S.L.

Genes Dev. 6, 2502-2512, 1992

Att: Isolation and characterization of protein-protein and protein-DNA interaction of GABRalpha an

A:Reference number: B46396

A:Accession: B46396

A:Molecule type: mRNA

A:Residues: 1-477 (BRO)

A:Cross-references: GB:110426; NID:q193195; PID:q515964

C:Superfamily: transcription factor EP81; ets DNA-binding domain homology

C:Keywords: DNA binding; nucleus; transcription factor

F:337-415/Domain: ets DNA-binding domain homology <ETS>

Query Match 4.2% Score 14; DB 1; Length 477;

Best Local Similarity 100.0%; Pred. No. 2, 6e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 KNPAMNYDKLSRS 308

DB 379 KNPAMNYDKLSRS 392

RESULT 4

S43692

N:Alternative names: ets variant gene 5; ets-related molecule

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 23-May-1997 #text_change 18-Sep-1998

C:Accession: S43692

R:Clon: 133 (Manning, M.; Karin, F.; Thummel, C.S.

Dev. Biol. 151, 176-191, 1992)

Att: Isolation and characterization of five Drosophila genes that encode an ets-rela

A:Reference number: S43692; MIM:94203669

A:Accession: S43692

A:Molecule type: mRNA

A:Residues: 1-510 (KON)

A:Cross-references: EMBL:X76184; NID:q479166; PID:q479167

C:Gene name

A:Gene: ERM44P

A:Cross-references: EMBL:X76184; NID:q479166; PID:q479167

C:Superfamily: ets DNA-binding domain homology

C:Keywords: DNA binding; nucleus; transcription factor

F:370-448/Domain: ets DNA-binding domain homology <ETS>

Query Match 4.2% Score 14; DB 1; Length 510;

Best Local Similarity 100.0%; Pred. No. 2, 4e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 KNPAMNYDKLSRS 308

DB 412 KNPAMNYDKLSRS 425

C:Superfamily: ets DNA-binding domain homology

C:Keywords: DNA binding; nucleus; transcription factor

F:370-448/Domain: ets DNA-binding domain homology <ETS>

RESULT 5
 S24051
 adenovirus E1A enhancer-binding protein E1AF - human (fragment)
 Nucleotide Accession: U01481, translation variant 4
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1993 #sequence_revision 23-May-1997 #text_change 18-Sep-1998
 C:Accession: U01481
 C:Status: preliminary
 A:Note: E1A, Yoshida, K., Fujinaga, Y., Kamio, K., Fujinaga, K., Nishida, A. J. Biol. Chem. 271: 547-553, 1996
 A:Cross-references: EMBL:U01481, NID:92161246
 A:Experimental source: HeLa cells
 A:Note: sequence extracted from NCBI backbone (NCBI:U01481, NCBI:U01481)
 C:Superfamily: E1A-1 transforming protein, ets DNA-binding domain homology
 C:Keywords: DNA binding
 F:7-65/Domain: ets DNA-binding domain homology <ETS>
 A:Cross-references: EMBL:U01481, NID:92161246, PID:92161246
 A:Accession: U01481
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-462 <DAL>
 A:Cross-references: EMBL:U01481, NID:92161246, PID:92161246
 A:Experimental source: HeLa cells
 A:Note: sequence extracted from NCBI backbone (NCBI:U01481, NCBI:U01481)
 C:Superfamily: E1A-1 transforming protein, ets DNA-binding domain homology
 C:Keywords: DNA binding
 F:7-65/Domain: ets DNA-binding domain homology <ETS>

Query Match 4.2% Score 14 DB 1 Length 453
 Best Local Similarity 100.0% Pred. No. 2.66-06
 Matches 14 Conservative 0 Mismatches 0 Indels 0 Gaps 0

DB 41 VARLMGIRKN 50
 S24051
 E1A enhancer-binding protein E1AF - human
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1993 #sequence_revision 23-May-1997 #text_change 05-Sep-1997
 C:Accession: U01481
 C:Status: preliminary
 A:Note: E1A, Yoshida, K., Fujinaga, Y., Kamio, K., Fujinaga, K., Nishida, A. J. Biol. Chem. 271: 547-553, 1996
 A:Cross-references: EMBL:U01481, NID:92161246, PID:92161246
 A:Experimental source: HeLa cells
 A:Note: sequence extracted from NCBI backbone (NCBI:U01481, NCBI:U01481)
 C:Superfamily: E1A-1 transforming protein, ets DNA-binding domain homology
 C:Keywords: DNA binding
 F:7-65/Domain: ets DNA-binding domain homology <ETS>

Query Match 4.2% Score 14 DB 1 Length 555
 Best Local Similarity 100.0% Pred. No. 3e-06
 Matches 14 Conservative 0 Mismatches 0 Indels 0 Gaps 0

DB 41 VARLMGIRKN 50
 S24051
 E1A enhancer-binding protein E1AF - human
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1993 #sequence_revision 23-May-1997 #text_change 05-Sep-1997
 C:Accession: U01481
 C:Status: preliminary
 A:Note: E1A, Yoshida, K., Fujinaga, Y., Kamio, K., Fujinaga, K., Nishida, A. J. Biol. Chem. 271: 547-553, 1996
 A:Cross-references: EMBL:U01481, NID:92161246, PID:92161246
 A:Experimental source: HeLa cells
 A:Note: sequence extracted from NCBI backbone (NCBI:U01481, NCBI:U01481)
 C:Superfamily: E1A-1 transforming protein, ets DNA-binding domain homology
 C:Keywords: DNA binding
 F:7-65/Domain: ets DNA-binding domain homology <ETS>

A:Title: Characterization of SAP-1, a protein recruited by serum response factor to t
 A:Reference number: A42093, M01D:92154673
 A:Accession: A42093
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-453 <DAL>
 A:Cross-references: EMBL:A42093, NID:92154673, PID:92154673
 A:Experimental source: HeLa cells
 A:Note: sequence extracted from NCBI backbone (NCBI:A42093, NCBI:A42093)
 C:Superfamily: E1A-1 transforming protein, ets DNA-binding domain homology
 C:Keywords: DNA binding
 F:7-65/Domain: ets DNA-binding domain homology <ETS>

Query Match 3.0% Score 10 DB 2 Length 453
 Best Local Similarity 100.0% Pred. No. 0.034
 Matches 10 Conservative 0 Mismatches 0 Indels 0 Gaps 0

DB 41 VARLMGIRKN 50
 S24051
 E1A enhancer-binding protein E1AF - human
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1993 #sequence_revision 23-May-1997 #text_change 05-Sep-1997
 C:Accession: U01481
 C:Status: preliminary
 A:Note: E1A, Yoshida, K., Fujinaga, Y., Kamio, K., Fujinaga, K., Nishida, A. J. Biol. Chem. 271: 547-553, 1996
 A:Cross-references: EMBL:U01481, NID:92161246, PID:92161246
 A:Experimental source: HeLa cells
 A:Note: sequence extracted from NCBI backbone (NCBI:U01481, NCBI:U01481)
 C:Superfamily: E1A-1 transforming protein, ets DNA-binding domain homology
 C:Keywords: DNA binding
 F:7-65/Domain: ets DNA-binding domain homology <ETS>

Query Match 3.0% Score 10 DB 2 Length 430
 Best Local Similarity 100.0% Pred. No. 0.033
 Matches 10 Conservative 0 Mismatches 0 Indels 0 Gaps 0

DB 41 VARLMGIRKN 50
 S24051
 E1A enhancer-binding protein E1AF - human
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1993 #sequence_revision 23-May-1997 #text_change 05-Sep-1997
 C:Accession: U01481
 C:Status: preliminary
 A:Note: E1A, Yoshida, K., Fujinaga, Y., Kamio, K., Fujinaga, K., Nishida, A. J. Biol. Chem. 271: 547-553, 1996
 A:Cross-references: EMBL:U01481, NID:92161246, PID:92161246
 A:Experimental source: HeLa cells
 A:Note: sequence extracted from NCBI backbone (NCBI:U01481, NCBI:U01481)
 C:Superfamily: E1A-1 transforming protein, ets DNA-binding domain homology
 C:Keywords: DNA binding
 F:7-65/Domain: ets DNA-binding domain homology <ETS>

Query Match: 4.0%, Score 10; DB 2; Length 405;
 Best Local Similarity: 100.0%; Pred. No. 0.031;
 Matches: 10; Conserved: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 300 MNYDKLSR 296
 |||||
 DB 11 VARIWIKRKN 50

RESULT 12
 Transferring protein etg-1; human
 N:Gene: etg-1; transforming protein etg-1; transforming protein etg-2
 C:Species: Homo sapiens (man)
 C:Date: Oct-1997 #sequence_revision 30-May-1997 #text_change 31-Oct-1997
 C:Accession: A44294; A44176; F58410; A28041; A29515
 C:Keywords: DNA binding; ets DNA-binding domain homology; ets RIT reg
 F:119-193/Domain: ets DNA-binding region homology <ETS2>
 F:312-396/Domain: ets DNA-binding domain homology <ETS>

A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-478 <DHO>
 A:Cross-references: EMBL:X77159; NID:q70439; PID:q70440
 C:Genetics:
 A:Gene: etg
 C:Superfamily: transcription factor etg; ets DNA-binding domain homology; ets RIT reg
 C:Keywords: DNA binding; phosphoprotein; proto-oncogene; transcription factor; transi
 F:119-193/Domain: ets DNA-binding region homology <ETS2>
 F:312-396/Domain: ets DNA-binding domain homology <ETS>

QY 300 MNYDKLSR 307
 |||||
 DB 359 MNYDKLSR 366

RESULT 12
 Transferring protein fil, long splice form - human
 N:Alternate names: Friend leukemia integration protein 1; transcription factor ERGB
 C:Species: Homo sapiens (man)
 C:Date: Oct-1997 #sequence_revision 30-May-1997 #text_change 20-Mar-1998
 C:Accession: L37565; S29843; S35506; A49000; A49015; L54170
 C:Deletions: O.; Zucman, J.; Plouastrel, B.; Desmartez, C.; Melot, T.; Peter, M.; Kovar,
 Nature 359, 162-165, 1992
 A:Title: Gene fusion with an ETS DNA-binding domain caused by chromosome translocatio
 A:Reference number: 137565
 A:Accession: 137565
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-452 <RES>
 A:Cross-references: EMBL:X67001; NID:q12529; PID:q12530
 F:17-65; P.; May, W.; Denny, C.; Paskind, W.; Moore, J.; Maki, R.A.; Brock, E.; Klems
 Biochim. Biophys. Acta 1172, 155-158, 1993
 A:Title: Human Fli-1 localizes to chromosome 11q24 and has an aberrant transcript in
 A:Reference number: S29843; MUID:q176499
 A:Accession: S29843
 A:Molecule type: mRNA
 A:Residues: 1-68; V.; 70-129; A.; 131-132; V.; 134-132; V.; 134-125; 427-452 <HRC2>
 A:Cross-references: EMBL:M93255
 A:Note: The authors translated the codon GTG for residue 69 as Gln
 F:17-65; P.A.; May, W.; Denny, C.; Paskind, W.; Moore, J.; Maki, R.A.; Brock, E.; Kle
 submitted to the EMBL Data Library, May 1993
 A:Description: Human Fli-1, an ETS oncogene family member preferentially expressed in
 A:Reference number: S35506
 A:Accession: S35506
 A:Molecule type: mRNA
 A:Residues: 1-68; V.; 70-76; 78-124; A.; 131-132; V.; 134-122; V.; 134-125; 427-452 <HRC2>
 A:Cross-references: EMBL:M93255; NID:q182559; PID:q182660
 F:17-65; P.D.; Rao, V.N.; Reddy, E.S.
 Cancer Res. 52, 5833-5837, 1992
 A:Title: Structure and expression of human Fli-1 gene.
 A:Reference number: A49000; MUID:q3007976
 A:Accession: A49000
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-322; V.; 324-452 <PPA>
 A:Cross-references: GB:S45205; NID:q257353; PID:q257354
 A:Note: sequence extracted from NCBI backbone (NCBI:115336; NCBI:115337)
 F:17-65; P.D.; Rao, V.N.; Reddy, E.S.; Thompson, D.M.; Chenu, J.O.; Testa, J.R.; Papas, T.S.; S
 Cell Growth Differ. 3, 705-713, 1992
 A:Title: The Ets/Fli-1 gene: isolation and characterization of a new member of the f
 A:Reference number: A49015; MUID:q3075640
 A:Accession: A49015
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-390; V.; 392-425; 427-452 <MAV>
 A:Cross-references: GB:M98833; NID:q182188; PID:q182189

Query Match: 2.4%, Score 8; DB 1; Length 478;
 Best Local Similarity: 100.0%; Pred. No. 4.2;
 Matches: 8; Conserved: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 300 MNYDKLSR 307
 |||||
 DB 359 MNYDKLSR 366

RESULT 12
 Transferring protein fil, long splice form - human
 N:Alternate names: Friend leukemia integration protein 1; transcription factor ERGB
 C:Species: Homo sapiens (man)
 C:Date: Oct-1997 #sequence_revision 30-May-1997 #text_change 20-Mar-1998
 C:Accession: L37565; S29843; S35506; A49000; A49015; L54170
 C:Deletions: O.; Zucman, J.; Plouastrel, B.; Desmartez, C.; Melot, T.; Peter, M.; Kovar,
 Nature 359, 162-165, 1992
 A:Title: Gene fusion with an ETS DNA-binding domain caused by chromosome translocatio
 A:Reference number: 137565
 A:Accession: 137565
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-452 <RES>
 A:Cross-references: EMBL:X67001; NID:q12529; PID:q12530
 F:17-65; P.; May, W.; Denny, C.; Paskind, W.; Moore, J.; Maki, R.A.; Brock, E.; Klems
 Biochim. Biophys. Acta 1172, 155-158, 1993
 A:Title: Human Fli-1 localizes to chromosome 11q24 and has an aberrant transcript in
 A:Reference number: S29843; MUID:q176499
 A:Accession: S29843
 A:Molecule type: mRNA
 A:Residues: 1-68; V.; 70-129; A.; 131-132; V.; 134-132; V.; 134-125; 427-452 <HRC2>
 A:Cross-references: EMBL:M93255
 A:Note: The authors translated the codon GTG for residue 69 as Gln
 F:17-65; P.A.; May, W.; Denny, C.; Paskind, W.; Moore, J.; Maki, R.A.; Brock, E.; Kle
 submitted to the EMBL Data Library, May 1993
 A:Description: Human Fli-1, an ETS oncogene family member preferentially expressed in
 A:Reference number: S35506
 A:Accession: S35506
 A:Molecule type: mRNA
 A:Residues: 1-68; V.; 70-76; 78-124; A.; 131-132; V.; 134-122; V.; 134-125; 427-452 <HRC2>
 A:Cross-references: EMBL:M93255; NID:q182559; PID:q182660
 F:17-65; P.D.; Rao, V.N.; Reddy, E.S.
 Cancer Res. 52, 5833-5837, 1992
 A:Title: Structure and expression of human Fli-1 gene.
 A:Reference number: A49000; MUID:q3007976
 A:Accession: A49000
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-322; V.; 324-452 <PPA>
 A:Cross-references: GB:S45205; NID:q257353; PID:q257354
 A:Note: sequence extracted from NCBI backbone (NCBI:115336; NCBI:115337)
 F:17-65; P.D.; Rao, V.N.; Reddy, E.S.; Thompson, D.M.; Chenu, J.O.; Testa, J.R.; Papas, T.S.; S
 Cell Growth Differ. 3, 705-713, 1992
 A:Title: The Ets/Fli-1 gene: isolation and characterization of a new member of the f
 A:Reference number: A49015; MUID:q3075640
 A:Accession: A49015
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-390; V.; 392-425; 427-452 <MAV>
 A:Cross-references: GB:M98833; NID:q182188; PID:q182189

[illegible]

```

misc_feature
    /note="MIP repeat: matches 146 / 76 of consensus"
    /complement(66137..66432)
    /note="match: GSS AG0666942"

repeat_region
    /note="M17D repeat: matches 553 / 1 of consensus"
    /note="MIP repeat: matches 553"
    /note="MIP repeat: matches 20 / 141 of consensus"
    /note="match: GSS P90081"
    /complement(72197..72557)

repeat_region
    /note="M17D repeat: matches 1 / 474 of consensus"
    /note="MIP repeat: matches 1"
    /complement(75287..75648)

repeat_region
    /note="THE1D repeat: matches 1 / 371 of consensus"
    /note="MIP repeat: matches 134 / 70 of consensus"
    /complement(76395..76458)

repeat_region
    /note="M17G repeat: matches 388 / 324 of consensus"
    /note="M17G repeat: matches 388"
    /complement(76658..76719)
    /note="M17D repeat: matches 553 / 505 of consensus"

Query Match      1.2%  Score 23  DB 9  Length 115835;
Best Local Similarity 100.0%  Pred. No. 0.4;
Methods 23  Conservative 0  Mismatches 0  Indels 0  Gaps 0.

cy 1505 ctgcctctgaaccttcagagccc 1546
      |||||||
Db 88123 ctgcctctgaaccttcagagccc 88102

PEPDUIT 12
MINNETN
LEOTUS
DEFINITION M.musculus net mRNA.
ACCESSION Z32815
NID 3479112
VERSION 232815.1 GI:479112
KEYWORDS Net: ras gene.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2658)
Giovane,A., Pintzas,A., Maira,S.M., Schieszczuk,P. and Wasyllyk,B.
Net: a negative factor switch to positive by Ras
Unpublished
2 (bases 1 to 2658)
Giovane,A.
Direct Submission
Submitted (29-APR-1994) Antoine Giovane
CHRS-LSME,INSEMG-U.184,Institut de Chimie Biologique, 11 rue
Humann, Strasbourg, 67085 Strasb. Cedex, France
3 (bases 1 to 2658)
Giovane,A., Pintzas,A., Maira,S.M., Schieszczuk,P. and Wasyllyk,B.
Net, a new ets transcription factor that is activated by Ras
Genes Dev. 8 (13), 1502-1513 (1994)
95047310

FEATURES
Source
Location/Qualifiers
1..2658
/organism="Mus musculus"
/db_xref="taxon:10090"
/dev_stage="10 days"
/tissue_type="embryo"
/clone_lib="lambda zap2"
295..1524
/codon_start=1
/product="Net"
/protein_id="CAA83676.1"
/db_xref="pid:9479113"
/db_xref="gi:479113"
/db_xref="MOL:MGI:101762"
/db_xref="SWISS-PROT:P41971"
/translation="MESKTIIMQPLHLHLIDPKHEHLTQWTSNDSDFELKAEVAKI
WELPNNKNNKNTPLSPAI PYYRNRKIFKVVQYFVAVKFSVFTLLKMPHAFVLSIS

```

ESLILDDGCKVSPPEVHRHPTLSLKASPNETHLSLYSTINLENFAFAKA
 IRLEKLEPHNSPVEEVIVIPVNTKTDHITPVKSLPSTISIAAASAPLAS
 SVAKISLMLPNAASVSSPSRSLSPDSPLSEHPLPFAACHSDSEPI
 NSSAKISKIKSPKPKPKLEISAPOLLISGDIISIALNSPALPSGSLTAFET
 AOTPSGLFLASPLPSIHFWSLSIPVAPLSPALQGPNTLFOFPTLLNGHMPVPLPS
 LDRAPSPVLSPSSOKS"

BASE COUNT 592 a 714 c 598 g 562 t
 ORIGIN

Query Match 100% Score 22 DB 12 Length 2659
 Best Local Similarity 100.00, Pred. No. 0.39,
 Matches 22, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 1312 catnaactacgacagctgagc 1333
 Db 450 CATNAACTACGACAGCTGAGC 474

RESULT 14
 LOCUS 882864 1526 bp mRNA ROD 19-FEB-1997
 DEFINITION Eukaryote, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ACCESSION S82864
 NID 81836129
 VERSION 1
 KEYWORDS Molecular cloning of Elk-3, a new member of the Ets family
 expressed during mouse embryogenesis and analysis of its
 transcriptional repression activity.
 SOURCE LNA Cell Biol 15 (1997) 855-865 (1997)
 ORGANISM Mus sp. 16-day embryos.

REFERENCE 1 (bases 1 to 1526)
 Nozaki, M., Onishi, Y., Kanno, N., Ono, Y. and Fujimura, Y.
 Molecular cloning of Elk-3, a new member of the Ets family
 expressed during mouse embryogenesis and analysis of its
 transcriptional repression activity.
 Lymphocyte development
 Mol. Cell. Biol. 17 (1997) 3292-3309 (1997)
 MEDLINE 94047916
 FEATURES
 location/Qualifiers
 1..1526
 /organism="Mus musculus"
 /strain="BALB/c"
 /sub_species="domesticus"
 /db_xref="taxon:10090"
 /sex="male"
 /tissue_type="lung"
 /tissue_id="lambda-911 of Clontech"
 302..3219
 /gene="Ets"
 322..1531
 /gene="Ets"
 /codon_start=1
 /protein_id="AA046893.1"
 /db_xref="PIR:G1836130"
 /db_xref="GI:1836130"

BASE COUNT 592 a 714 c 598 g 562 t
 ORIGIN

Query Match 100% Score 22 DB 12 Length 2659
 Best Local Similarity 100.00, Pred. No. 0.39,
 Matches 22, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 1312 catnaactacgacagctgagc 1333
 Db 450 CATNAACTACGACAGCTGAGC 481

RESULT 14
 LOCUS 882864 1526 bp mRNA ROD 19-FEB-1997
 DEFINITION Eukaryote, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ACCESSION S82864
 NID 81836129
 VERSION 1
 KEYWORDS Molecular cloning of Elk-3, a new member of the Ets family
 expressed during mouse embryogenesis and analysis of its
 transcriptional repression activity.
 SOURCE LNA Cell Biol 15 (1997) 855-865 (1997)
 ORGANISM Mus sp. 16-day embryos.

REFERENCE 1 (bases 1 to 1526)
 Nozaki, M., Onishi, Y., Kanno, N., Ono, Y. and Fujimura, Y.
 Molecular cloning of Elk-3, a new member of the Ets family
 expressed during mouse embryogenesis and analysis of its
 transcriptional repression activity.
 Lymphocyte development
 Mol. Cell. Biol. 17 (1997) 3292-3309 (1997)
 MEDLINE 94047916
 FEATURES
 location/Qualifiers
 1..1526
 /organism="Mus sp."
 /db_xref="taxon:10095"
 94..1323
 /gene="Elk-3"
 94..1323
 /gene="Elk-3"
 /note="Ets transcription factor. This sequence comes from
 Fig. 1"

BASE COUNT 592 a 714 c 598 g 562 t
 ORIGIN

Query Match 100% Score 22 DB 12 Length 2659
 Best Local Similarity 100.00, Pred. No. 0.39,
 Matches 22, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 1312 catnaactacgacagctgagc 1333
 Db 450 CATNAACTACGACAGCTGAGC 273

RESULT 15
 LOCUS PFMA13P4/c 113899 bp DNA INV 29-APR-1999
 DEFINITION Plasmodium falciparum MAL3P4, complete sequence.
 ACCESSION AL008970

[illegible]

ALIGNMENT'S

[illegible]

REF: 1
AF071546
LOCUS: 14q24
DEFINITION: Human salivary IgA transcription factor PDEF (PDEF) mRNA, complete cds.
ACCESSION: AF071546
MIM: 14007417
VERSION: 1
KEYWORDS: Salivary
SOURCE: Human
ORGANISM: Homo sapiens
PubMed: 7443644
Publication: M. and A. Choudhry, Granulata; Vertebrata, Mammalia, Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 1894)
Author(s): Finger E., Akbarally, Y., Tharongsak, U., Dube, A., Holtax, J., Brown, L., Kunsch, C. and Lieberman, T.A.
Title: Isolation and characterization of a novel prostate epithelium-specific Ets transcription factor, PDEF
Unpublished
2 (bases 1 to 1894)
Author(s): Lieberman, T.A., Choudhry, P., Kunsch, C. and Finger, E.
Title: Direct Submission
Journal: Submitted (JUN-1998) Medicine, Beth Israel Deaconess Medical Center, 740 Brookline Ave., Boston, MA 02115, USA
Features: 1..1894

```

/organism:"Homo sapiens"
/chr:"1"
/chr_pos:"35000000"
/chromosome:"6"
/feat:"CpG"
/feature_type:"prostate"
/issue:"1004"
/anno:"pindel"

```

[illegible]

AF0076706 848 bp mRNA VPT 19-DEC-1998
 LOCATION: Gallus gallus ois domain protein (ERM) mRNA, partial cds.
 DEFINITION: AF0076706
 ACCESSION: AF0076706
 MID: AF0076706.1 (1:486457)
 KEYWORDS:
 ORGANISM: Gallus gallus
 Eukaryote; No group; Chordata; Craniata; Vertebrata; Archosauria;
 Aves; Neornithes; Galliformes; Phasianidae; Phasianinae; Gallus.
 REFERENCE: 1 (bases 1 to 848)
 AUTHORS: Lin, J.H., Salto, T., Anderson, D.J., Lance-Jones, C., Jessell, T.M. and
 Atherton, S.
 TITLE: Functionally related motor neuron pool and muscle sensory afferent
 subtypes defined by coordinate ETS gene expression
 JOURNAL: Cell 95 (3): 393-407 (1998)
 MEDLINE: 99029846
 REFERENCE: 2 (bases 1 to 848)
 AUTHORS: Lin, J.H., Salto, T., Anderson, D.J., Lance-Jones, C., Jessell, T.M. and
 Atherton, S.
 TITLE: Direct Submission
 JOURNAL: Submitted (01-JUL-1998) Center for Neurobiology & Behavior,
 Columbia University, 701 W. 168th St. HHSC 1013, New York, NY
 10032, USA
 FEATURES:
 location/qualifiers
 1..848
 /organism="Gallus gallus"
 /db_xref="taxon:9031"
 /gene="ERM"
 /locus_tag="AAC97203.1"
 /protein_id="P40337.65"
 /translation="VHNNHRIIVLYLDFSPSAVDPPRYGKSPPGTPIQSPFQF
 PRODRNLTSPGPHPTSMGYLIENSSAYQAVAPAVIKQEVPMYMSGSKOMKPF
 SEQCIQCPQGFKEFHDPGEYAGPSCYPAVAVIKQEVPMYMSGSKOMKPF
 ADDCVYPERKEFDIKQEGVREGPRGPGSLQMOELVATIDPITSHTAFTGR
 GMERLTPEPVAKMGIOKRPAMNYDKISPTPYEKGIMQAKGPPYKRYCE
 PEALFSLAFPNLPPALKALFLFQISITIVPLSHLSTAVIPGLNSTPGLVQNGY
 TY"
 BASE COUNT 563 a 715 c 672 g 557 t 1 others
 ORIGIN
 Query Match 1.5% Score 30; DB 4; Length 2508;
 Best Local Similarity 100.0%; Pred. No. 136-05;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Unordered pieces
 ACCESSION AC007818
 MID 95053146
 VERSION AC007818.1 GI:5053146
 HTG: HTGS_PHASE1.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachyera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 60056)
 AUTHORS: Celniker, S.E., Abmayyan, A., Arcaina, T.T., Baxter, E., Blazek, R.G.,
 Butenhoff, C., Champe, M., Chavez, C., Chow, M., Ciolek, L.,
 Doyle, C.M., Farfan, D.F., Galle, P., George, R.A., Harris, N.L.,
 Hoskins, P.A., Houston, K.A., Humastis, S.P., Kara, K., Kearney, L.,
 Kim, E., Lee, B., Lewis, S., Li, P., Lomtan, M.A., Mada, P.,
 Mosher, A.P., Moshrefi, M., Nixon, K., Pajlab, T.M., Park, S.,
 Pfeiffer, B., Poon, L., Sequerra, A., Sethi, R., Smit, E.,
 Switskas, P.P., Wan, X.H., Weinburg, J., Zhang, R., Zietan, L.L. and
 Rubin, G.M.
 TITLE: Sequencing of Drosophila melanogaster
 JOURNAL: Unpublished
 REFERENCE: 2 (bases 1 to 60056)
 AUTHORS: Celniker, S.E., Abmayyan, A., Arcaina, T.T., Baxter, E., Blazek, R.G.,
 Butenhoff, C., Champe, M., Chavez, C., Chow, M., Ciolek, L.,

JOURNAL Cell 95 (3): 393-407 (1998)
 MEDLINE 99029846
 REFERENCE 2 (bases 1 to 2508)
 AUTHORS: Lin, J.H., Salto, T., Anderson, D.J., Lance-Jones, C., Jessell, T.M. and
 Atherton, S.
 TITLE: Direct Submission
 JOURNAL: Submitted (01-JUL-1998) Center for Neurobiology & Behavior,
 Columbia University, 701 W. 168th St. HHSC 1013, New York, NY
 10032, USA
 On Nov 19, 1998 this sequence version replaced GI:386456.
 COMMENT Location/Qualifiers
 1..2508
 /organism="Gallus gallus"
 /db_xref="taxon:9031"
 <1..2508
 /gene="PEA3"
 <1..1011
 /gene="PEA3"
 /codon_start=1
 /product="ets domain protein"
 /protein_id="AAC97203.1"
 /db_xref="P40337.65"
 /db_xref="GI:4033765"
 /translation="VHNNHRIIVLYLDFSPSAVDPPRYGKSPPGTPIQSPFQF
 PRODRNLTSPGPHPTSMGYLIENSSAYQAVAPAVIKQEVPMYMSGSKOMKPF
 SEQCIQCPQGFKEFHDPGEYAGPSCYPAVAVIKQEVPMYMSGSKOMKPF
 ADDCVYPERKEFDIKQEGVREGPRGPGSLQMOELVATIDPITSHTAFTGR
 GMERLTPEPVAKMGIOKRPAMNYDKISPTPYEKGIMQAKGPPYKRYCE
 PEALFSLAFPNLPPALKALFLFQISITIVPLSHLSTAVIPGLNSTPGLVQNGY
 TY"
 BASE COUNT 563 a 715 c 672 g 557 t 1 others
 ORIGIN
 Query Match 1.5% Score 29; DB 4; Length 2508;
 Best Local Similarity 100.0%; Pred. No. 4.8e-05;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Unordered pieces
 ACCESSION AC007818
 MID 95053146
 VERSION AC007818.1 GI:5053146
 HTG: HTGS_PHASE1.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachyera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 60056)
 AUTHORS: Celniker, S.E., Abmayyan, A., Arcaina, T.T., Baxter, E., Blazek, R.G.,
 Butenhoff, C., Champe, M., Chavez, C., Chow, M., Ciolek, L.,
 Doyle, C.M., Farfan, D.F., Galle, P., George, R.A., Harris, N.L.,
 Hoskins, P.A., Houston, K.A., Humastis, S.P., Kara, K., Kearney, L.,
 Kim, E., Lee, B., Lewis, S., Li, P., Lomtan, M.A., Mada, P.,
 Mosher, A.P., Moshrefi, M., Nixon, K., Pajlab, T.M., Park, S.,
 Pfeiffer, B., Poon, L., Sequerra, A., Sethi, R., Smit, E.,
 Switskas, P.P., Wan, X.H., Weinburg, J., Zhang, R., Zietan, L.L. and
 Rubin, G.M.
 TITLE: Sequencing of Drosophila melanogaster
 JOURNAL: Unpublished
 REFERENCE: 2 (bases 1 to 60056)
 AUTHORS: Celniker, S.E., Abmayyan, A., Arcaina, T.T., Baxter, E., Blazek, R.G.,
 Butenhoff, C., Champe, M., Chavez, C., Chow, M., Ciolek, L.,

[illegible]

```

TITLE Direct Submission
JOURNAL JOURNAL
26 Rue Daum, Paris 75231 Cedex 05, Paris 75231 Cedex 05, FRANCE
FEATURES
    source
        location/Qualifiers
            1..1901
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /chromosome="2"
                /cell_line="ewing"
            585..1301
                /function="DNA binding protein"
                /note="ETS family member"
                /codon_start=1
                /product="FEV protein"
                /protein_id="CA70169.1"
                /db_xref="PID:e291921"
                /db_xref="PID:g1834509"
                /db_xref="GI:1834509"
                /db_xref="SPTREML:Q99581"
                /translation="MRQSGAPLLINMYIPNVGNGLEFKGSKNPDSWSPJLSPAVCKSS
                GOIQWQFLELELADRANAGCIAMEGHSEFKLTDPDEVARRWGEFRKSPMYNDKLS
                RLPRVYVKNKINSVVKHGRPYAFEDFGLAQACPPPAHAAAAAAGAAAAAAGDGL
                YLPLPGLAPLEPGLSKLNTLMAASAGVAPAGSYMPGPPAPATAATAATLYPSPDQ
                PPGSPFGVAAASHSGHYH"
            711..962
                /note="DNA binding domain"
BASE COUNT      302 a      707 c      575 g      317 t
ORIGIN
Query Match      1.3% Score 25; DB 10; Length 1901;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Cy 1312 catgaactacgacaagctgagccgc 1336
|||||
Db 869 CATGACTACGACACGCTGAGCCGC 893
|||||
DEFINITION
PROTEIN 480 bp RNA INV 05-APR-1992
Drosophila melanogaster D-ets-6 DNA binding domain protein gene,
partial cds.
ACCESSION
M88475
VERSION
M88475.1 GI:157197
KEYWORDS
DNA-binding domain protein.
Drosophila melanogaster DNA.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 480)
Chen, T.; Bunting, M.; Karim, F. D. and Thummel, C. S.
Isolation and characterization of five Drosophila genes that encode
an ets-related DNA binding domain
Dev. Biol. 151, 176-191 (1992)
JOURNAL MEDLINE
DEV 92249640
FEATURES
    source
        location/Qualifiers
            1..480
                /organism="Drosophila melanogaster"
                /db_xref="taxon:7227"
                /map="Chromosome 2L 21C."
            1..95
                /gene="D-ets-6 DNA-binding domain"
            96..288
                /gene="Ets21C"
                /db_xref="Flybase:FBgn005660"
            join(96..288,366..480)
                /gene="Ets21C"
                /note="Ets at 21C"
                /allele=""

```


[illegible]

[illegible]

```

Query Match      1.28: Score 22: DB 12: Length 2658:
Best Local Similarity 100.0%: Pred. No. 0.39:
Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1312 catgaactacgacaagctgagc 1333
|||||
DB 453 CATGAACCTACGACAACTGAGC 474

RESULT 13
MUSTRANONC
LOCUS MUSTRANONC 2211 bp mRNA 19-III-1994
DEFINITION Mus musculus ERP mRNA, complete cds.
ACCESSION L19953
MID 9436184
VERSION 119953.1 GI:436184
KEYWORDS transcription factor.
SOURCE Mus musculus (strain BALB/c, sub-species domesticus) (library:
lambda-gtl1 of Clontech) male lung cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2211)
AUTHORS Lopez,M., Oetgen,P., Akbarali,Y., Dendorfer,U. and Lhermann,T.A.
TITLE ERP, a new member of the ets transcription factor/oncoprotein
family, cloning, characterization, and differential expression
during B-lymphocyte development
Mol. Cell. Biol. 14 (5): 3292-3309 (1994)
34217726
FEATURES
Source
Location/Qualifiers
1..2211
/organism="Mus musculus"
/strain="BALB/c"
/sub_species="domesticus"
/db_xref="taxon:10090"
/sex="male"
/tissue_type="lung"
/tissue_lib="lambda-gtl1 of Clontech"
302..2199
/gene="ERP"
302..1531
/gene="ERP"
/codon_start=1
/protein_10="AA136872.1"
/db_xref="PIR:g436185"
/db_xref="GI:436185"
/translation="MESAITLMQFLHLILNOKHEHJQWTSNDGQFKI:KAEYAKI:
KQILPQKINMWNK:SPALPYVYKNIKKVIOQKVFVFSFPI:KMDPVAV:ISKQ:
EELLQDDQCVKSPGEGPQVHGLSLKASAPNEYLHSGIYSSPTINSIQNAPKFKR:
ITKELEPPQDSDPPEVPTVTFVFNKDKMTPTPMSSTSTIAAASAAFLAA:
SVSAATSLKLPMAKVSASAPSSSPSPSI:SPSP:PSHRELI:FAACHHDSLEP:
NISSSSKLSKSPSLPPKGRGLEISAPQLLSGTIDGSIALSSALPSGSLTPAFF:
AOTPGSLTASPLPS:HFWSSTLSVAPISPARLQGPNTLQPIILLNGHMPVLP:
LDRAPSPVLLSPSSQKS"
320..553
/gene="ERP"
/note="ETS domain"
2195..2199
/gene="ERP"
misc_feature
polyA_signal
polyA_signal
BASE COUNT 560 a 513 c 504 g 514 t
ORIGIN
Query Match      1.28: Score 22: DB 12: Length 2211:
Best Local Similarity 100.0%: Pred. No. 0.49:
Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1312 catgaactacgacaagctgagc 1333
|||||
DB 460 CATGAACCTACGACAACTGAGC 481

```




A:Reference number: 158410; MUID:94119611
A:Accession: 158410
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Accession: Z94-279; RES.
A:Organism: Drosophila obscura; NID:q544960; PID:q544961
A:Gene: DBEPI
A:Gene accession: DBEPI19884; OMIM:165080
A:Map position: c12r,c12r,c12r
A:Map position: c12r,c12r,c12r
C:Specialty: transcription factor ets; ets DNA-binding domain homology; ets P1 region
C:Keywords: alternative splicing; DNA binding; nucleus; proto-oncogene; transcription factor
F1:Z94-279/486/Protein; transforming protein ets-1 status predicted <ES>
F1:Z94-279/486/Protein; transforming protein ets-1 status predicted <EC1>
F1:Z94-279/486/Protein; transforming protein ets-1 status predicted <EC2>
F1:Z94-279/486/Protein; transforming protein ets-1 status predicted <EC3>
F1:Z94-279/486/Protein; transforming protein ets-1 status predicted <EC4>
F1:Z94-279/486/Protein; transforming protein ets-1 status predicted <EC5>

Query Match 16/94 Score 302.5; DB:1 Length 486;
Best Local Similarity 26.0%; Pred. No. 1.6e-17;
Matches 106; Conservative 45; Mismatches 121; Indels 135; Gaps 16;

CY 15 ESPALPEGLSAS-----YLSEFLML-----YPEDSSWAKAPASSPE 84
DB 6 LTPAAHIFALSVSHRSLTCLAYGTPLAKTEHTASSSDCGTSKMSRFVQDDLS 65
CY 66 RRP-----EPPECVINSQADAGSLDLP---GGLTEHSLECVQ 123
DB 66 TFAVITIKMFNPSQVNSENSPREGSAVKGGKVGSPTGYNNYSMEEKHW--PP 123
CY 134 SNAVREVLKDTLAKLINILAIWDMSNSYOKMLTETHOYRLPMG-KAFOLAKE 182
DB 134 NTTFN-----RRVVADPDLKSTDHVRLMAVKEVGLDYNIILLFONIDKE 174
CY 184 DAVMSDFPKPSI-LGVVIAHL-----DIWK-----SAAMKEPTSPA 223
DB 174 LKKMKIDQDETFSYNAIIISLLHYLETPLPLTSDVDKALQNSPRLMHANTGA 234
CY 234 TRVANSIS-----ESSM----- 236
DB 234 AETFINNVPAIQRIIRMLPYEPFRKSAMTGHPGPSKAADPSSTVPKTEDQR 294
CY 294 -----EDSVDSNSGCPRIHMQLFKELKHSVSPTFRMWLNKEGIKIDS 284
DB 294 TCDIVYGTLGPISSKLANPSSGO-IQIMOFFLE-LLSDSSNSSCITW-EQTNGEKMTDP 351
CY 354 AVANVWLTPREFARNKLTFSIPVYKKLIKPRTSDPLVYGF 311
DB 354 LVAARWGHFGRKRNKLTFSIPVYKKLIKPRTSDPLVYGF 327

RESUT
SVTCT
Transcription factor ets-1 fruit fly (Drosophila melanogaster)
N/A:Reference name: transcription factor ets-97D
C:Species: Drosophila melanogaster
C:Date: 14 Jan 1995; Revision: 23 May 1997 #text_change 18-Sep-1998
C:Accession: S87616; S88822
R:Title: S.M.T. Xiao, X.L. Feng, F.S. Pang, T.S. Watson, D.K. Schultz, F.A.
Cheng, et al., 1992
ATT:et-1 encodes a putative transcription factor involved in structural organization of D-elig, an ets proto-oncogene
A:Reference number: S87616; MUID:93096481
A:Accession: S87616
AST:Gene: Preliminary
AST:Gene type: DNA
A:Molecule type: DNA
A:Accession: I-464; THE
A:Cross reference: EMBL:X8579; NID:q7942; PID:q7943
Richard, J.J. Montano, M.J. Failing, F.L. Thummler, C.S.
Dev. Biol. 151, 176-191, 1992
ATT:et-1 encodes a putative transcription factor involved in structural organization of five Drosophila genes that encode an ets-rela
A:Reference number: S88822; MUID:92249640
A:Accession: S88822
A:Molecule type: mRNA

```

A:Residues: 298-449 <CHE>
A:Cross-references: EMBL:M88471; NID:9157189; PID:9552088
A>Note: the authors translated the codon AGC for residue 302 as Thr
C:Genetics:
A:Gene: FLYBase:Ets97D
A:Cross-references: FLYBase:FBgn0004510
A:Annotations: 22/1: 60/2: 83/3: 322/1
C:Superfamily: transcription factor elg; ets DNA-binding domain homology; ets RII reg
C:Keywords: DNA binding; nucleus; transcription factor
F:190-253/Domain: ets RII regulatory region homology <ERP>
F:348-456/Domain: ets DNA-binding domain homology <ETS>

Query Match 16.5% Score 294; DB 1; Length 464;
Best Local Similarity 29.1% Pred. No. 7.5e-17;
Matches 92; Conservative 52; Mismatches 116; Indels 56; Gaps 12;

QY 64 DMLVDESDSMKAKPAGASREPEPEQCVIDSOAPAGSLDLVPGSLTEHSLEQV 123
DB 118 DLVAKTEALALAEVYGQLSPETASQ-----KSSSESIRKPLPKMHEDSEDEVE 173
QY 124 SMVGEVLK-DIEACK---LNTIADPMDSNSVOKMLMTEHOYRLPPMKAPDEL 178
DB 124 GKDVPLVNLWVDSKFRQRIKLPKANEMTHAHVYLEMVAKGELVGNMSDWQM 233
QY 179 ACKELANSEDFQPPRSPLG-GDVHAHLDLMKSAAM-----KERTSP----- 222
DB 234 NQCELCAMTHFEFNOKLPDPDNIFMTLQLIKCEQVSVYVKKAEDEKPKPRIMSAN 293
QY 222 -----GAI-----HVCASSTSESMTDS-----EVESCSQCPHLWQFL 255
DB 294 SINTSGGSLSLQPIPKSYQSVKSSDSVESTTSMNPSVYTTIGSSNNQ-VQIMQFL 352
QY 256 KELLKPHSYGRFIFWLKKEGKEIKEDSAGVAPLWIPKMPAMNYTKLSPLSPYVYKK 315
DB 353 LE-ILTDEHNTDVEIEMVGE-GEFKLTDPPDVARLWGRKKPKPAMNYFKI SPAL RYVYVYG 410
QY 316 GIIKKPDISQRLVYQF 331
DB 411 DMISKVS-GKRPAYKF 425

RESULT 4
138739
nuclear respiratory factor-2 subunit alpha - human
C:Species: Homo sapiens (man)
C:Accession: U03044; NID:9571892; E:05531893
C:Accession: 1-454 <RES>
F:348-456/Domain: ets RII regulatory region homology <ERP>
F:124-245/Domain: ets RII regulatory region homology <ETS>
F:322-450/Domain: ets DNA-binding domain homology <ETS>
A:Status: preliminary; translated from GR/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-454 <RES>
A:Cross-references: EMBL:U03044; NID:9571892; E:05531893
C:Superfamily: transcription factor elg; ets DNA-binding domain homology; ets RII reg
F:124-245/Domain: ets RII regulatory region homology <ERP>
F:322-450/Domain: ets DNA-binding domain homology <ETS>

Query Match 16.4% Score 293; DB 2; Length 454;
Best Local Similarity 28.1% Pred. No. 8.8e-17;
Matches 86; Conservative 49; Mismatches 125; Indels 46; Gaps 9;

QY 60 LSYFPMVLPEDSSMAKAPGASREPEPEPEQCPIYNSQAPAGSLDLVPGSLTEHSL 119
DB 108 LNLIVRPADIVVEVVIDPDAAHASEAHVLEEAVI-----LIDTQKHITTSDETS 160
QY 120 ENYGVSMVWSEVTKDLETKNLNLTADPMLESPSNVGMWLLWIEHYLYLPPMGAKF/ELA 179
DB 161 EGVYTMAA--ALEGTRKDEERGLIYFDIOWSTVDYLVHVVWVWAKFESMTDITLTINIS 218

```


DB 005474794.400

RESULT

A:Gene: ets-1

C:Superfamily: transcription factor ets-1; ets DNA-binding domain homology; ets RII reg

C:Keywords: DNA binding; nucleus; proto-oncogene; transcription factor; transforming

F:117-191/Domain: ets RII regulatory region homology <ETS2>

F:287-362/Domain: ets DNA-binding domain homology <ETS>

A:Accession: M20507

A:Reference: 1485 <EAT>

A:Cross-references: GB M20507, GB M20508, GB M20509, GB M20510, GB M20511, GB M20512,

A:Gene: ets-1

C:Superfamily: transcription factor ets; ets DNA-binding domain homology; ets RII reg

C:Keywords: alternative splicing; DNA binding; nucleus; proto-oncogene; transcription

F:101-174/Domain: ets RII regulatory region homology <ETS2>

F:381-459/Domain: ets DNA-binding domain homology <ETS>

F:421-427/Region: nuclear location signal

Query Match 15.54; Score 277; DB 1; Length 453;

Best Local Similarity 32.4%; Pred. No. 1,99-15;

Matches 78; Conservative 29; Mismatches 78; Indels 56; Gaps 9;

DB 125 VPAADPALSGDHPQWLEMAIKKEGLVEIDCSLFGWIKELCKSKRPFLLSTNYTF 184

DB 221 VLAHLDJIKWSAA.....WMEERTF222

DB 185 VLSHLNVLDPSSSLGYNFQAHDPSPITAKEPSEYFAVPSGNGNSPVTKSPM 244

DB 222 GAHYCASTEESW.....IDSEVDSGSCGPHLMWFLKELLKRYGRTIP 270

DB 245 GGTGKVKSGDQQRSCDFPYQILGPTSSPLANGSGQ...IQWQFLE...CISGSSVASTT 302

DB 271 WLNEKGIETKEDSAQVARYLGRKRPANNDKLSRSIRYQKGIJRPDISRLVYQ 330

DB 303 W-ETNGPFRKTPDEEVAPWDEPKSKFNKNYKLSFALPYRYSTKTVH-CPPVAVK 360

DB 331 F 331

DB 361 F 361

RESULT 9

Transcription factor ets-1, splice form b - chicken

C:Species: Gallus gallus (chicken)

C:Date: 31-Dec-1999 #sequence-revision 31-Dec-1999 #text-change 30-May-1997

A:Accession: A28875; A28610

A:Reference: D: Duterque-Cogulland, M. J.; R.P.; Henry, G.; Flouris, A.; Debure,

A:Title: Alternative splicing within the chicken c-ets-1 locus: implications for tran

A:Reference number: A28875; M01D:88300873

A:Accession: A28875

A:Residues: 1-485 <LEP>

C:Genetics:

A:Gene: ets-1

C:Superfamily: transcription factor ets; ets DNA-binding domain homology; ets RII reg

C:Keywords: DNA binding; nucleus; proto-oncogene; transcription factor; transforming

F:117-191/Domain: ets RII regulatory region homology <ETS2>

F:287-362/Domain: ets DNA-binding domain homology <ETS>

A:Accession: M20507

A:Reference: 1485 <EAT>

A:Cross-references: GB M20507, GB M20508, GB M20509, GB M20510, GB M20511, GB M20512,

A:Gene: ets-1

C:Superfamily: transcription factor ets; ets DNA-binding domain homology; ets RII reg

C:Keywords: alternative splicing; DNA binding; nucleus; proto-oncogene; transcription

F:101-174/Domain: ets RII regulatory region homology <ETS2>

F:381-459/Domain: ets DNA-binding domain homology <ETS>

F:421-427/Region: nuclear location signal

Query Match 15.28; Score 272; DB 1; Length 485;

Best Local Similarity 24.7%; Pred. No. 5,39-15;

Matches 112; Conservative 42; Mismatches 109; Indels 200; Gaps 18;

DB 65 MLYPDSSMAKAP.....GASSREPEEP.....ECPYIDSCA---101

DB 2 MSYWDITISTSPYPLAFPMV...GASSQTEPPWMTKLSACCPSPFWDFAIOE 61

[illegible][illegible]

```

D6      213 PLANKEDPSYDVBPGAMNNNNNNGLKSPILGSGQWCKNTQTPQPPQPPQYILCTPTSS - 271
QY      234 SWLDEYDSSCSGQPHLMQCFKELLKFNHYSGFTLWLNKEKGIKIDTSVVARLWGI 291
D6      271 ----SPLANGSGQ--QQLMQLFILELDESSNAGCTIW-EGTNGEKKMTTPFVAFRPGSE 321
QY      294 PRNPANWERTKISRSPQYKKKGTIRKEDISQPLVQF 331
D6      324 PRKSPNNNTKLSRALPYDYDNTIKYH--GRAPAYVF 360

```

transforming protein flt-1 long splice form - human
Nucleotide names: Friend leukemia integration protein 1: transcription factor EFG8
C.Species: Homo sapiens (man)
C.Date: 04-Oct-1996 #sequence-revision 30-May-1997 #text-change 20-Mar-1998
A.Accession: U17565; S29843; S3506; A49000; A49015; U54170
R.Delattre, O. Zucman, J. Ploegastel, B. Desnaze, C. Melot, T. Peter, M. Kovar,
Nature 359, 162-165, 1992

A.flt1: Gene fusion with an ETS DNA-binding domain caused by chromosome translocation
A.Reference number: 137378, MVID 9239239

A.Accession: U17565

A.Status: Preliminary; translated from GE/EMBL/DBJ

A.Molecule type: mRNA

A.Peslides: 1-452 <RES>

A.Cross-references: EMBL:X67001, NID:Q32279, PID:Q25330

R.Horras, F. May, W. Denny, C. Pasikind, W. Moore, J. Maki, R.A. Beck, E. Klein,
Biochim. Biophys. Acta 1172, 155-158, 1993

A.flt1: Human FLT-1 localizes to chromosome 11q24 and has an aberrant transcript in
A.Reference number: S29843; MUID:93176799

A.Accession: S29843

A.Molecule type: mRNA

A.Peslides: 1-62, V. 70-129, A. 121-132, V. 133-132, Q. 134-425, 427-472 <HPD2>

A.Cross-references: EMBL:M93255

A.Note: The authors translated the codon GTG for residue 69 as GUG

R.Horras, F. A. May, W. Denny, C. Pasikind, W. Moore, J. Maki, R.A. Beck, E. Klein
Submitted to the EMBL Data Library, May 1993

A.Description: Human FLT-1, an ETS oncogene family member preferentially expressed in
A.Reference number: S35506

A.Accession: S35506

A.Molecule type: mRNA

A.Peslides: 1-68, V. 70-76, 78-129, A. 131-132, V. 134-132, Q. 134-425, 427-472 <HPD2>

A.Cross-references: EMBL:M93255, NID:Q182659; PID:Q182660

R.Prasad, D. D. Rao, V.N.; Reddy, E.S.

Cancer Res. 52, 5835-5837, 1992

A.flt1: Structure and expression of human Flt-1 gene.
A.Reference number: A49000, MUID:93007976

A.Accession: A49000

A>Status: Preliminary

A.Molecule type: mRNA

A.Peslides: 1-122, C. 324-452 <PFA>

A.Cross-references: GB:S45235, NID:J257353, PID:Q25334

A.Note: sequence extracted from NCBI backbone (NCRI:U115336, NCRI:P:115337)

P.Watson, D.K.; Smith, P.E.; Thompson, D.M.; Cheng, J.O.; Testa, J.R.; Papas, T.S.; S
Cell Growth Differ. 3, 705-713, 1992

A.flt1: The EGFRL/Flt-1 gene: isolation and characterization of a new member of the f
A.Reference number: A49015, MVID:93075640

A.Accession: A49015

A.Status: Preliminary

A.Molecule type: mRNA

A.Peslides: 1-390, C. 392-425, 427-452 <MAT>

A.Cross-references: GB:M98833; NID:Q182188; PID:Q182189

A.Note: sequence extracted from NCBI backbone (NCRI:U119390, NCRI:P:119392)

R.Rand, V. Lilienski, W. Passart, E.J. Poliquin, L. Bergeron, D.
Genomics 11, 223-224, 1991

A.flt1: The human homolog of the mouse common viral integration region, Flt1, maps t
A.Reference number: U54170; MVID 9239239

A.Accession: U54170

A.Status: Preliminary; nucleic acid sequence not shown; translated from SE/EMBL/DBJ

A.Molecule type: DNA

A.Peslides: 1-6 +PE2>

